

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 99177

**TO: Rebecca Prouty** 

Location: cm-1/10a13/10d01

Art Unit: 1652

Friday, August 01, 2003

Case Serial Number: 10/089986

From: Toby Port

**Location: Biotech-Chem Library** 

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

### Search Notes

Dear Examiner Prouty,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 

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Sequence 6109, Ap
Sequence 15653, A
Sequence 8453, Ap
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Sequence 1
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO0_DUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO0_RUM_PUB.seq:*
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version 5.1.6
- 2003 Compugen Ltd.
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US-09-960-352-6109
US-09-918-995-15653
US-09-960-352-8453
US-10-239-676-209
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Maximum Match 1008
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                                                      nucleic search, using sw model
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Sequence 5, Appli
Sequence 1, Appli
Sequence 142839,
Sequence 34, Appli
Sequence 4021, Ap
Sequence 37, Appl
Sequence 27, Appli
Sequence 24, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 34, Appli
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Sequence 33842, A
Sequence 6502, Ap
Sequence 71236, A
Sequence 71236, A
Sequence 71236, A
Sequence 7284, A
Sequence 7284, A
                           Sequence 551, Appl Sequence 1, Appli Sequence 259845, Sequence 4627, Appli Sequence 24, Appli Sequence 137361,
                                                                                                                         Sequence 206, App
Sequence 261, App
Sequence 33841, A
    3, Appl
33098,
2 US-09-995-898A-28

US-08-719-986A-51

US-08-719-986A-51

US-09-790-988-1

US-09-938-842A-4627

US-09-938-842A-4627

US-09-938-842A-4627

US-09-938-842A-4627

US-00-027-632-33841

US-10-027-632-33842

US-10-027-632-33842

US-10-027-632-33842

US-10-027-632-33842

US-10-027-632-33842

US-09-10-027-632-33842

US-09-10-027-632-33842

US-09-10-027-632-1236

US-10-027-632-1236

US-10-027-632-1238

US-09-815-242-6598

US-09-815-242-6598

US-09-815-242-6598

US-09-818-320-3

US-09-938-842A-4021

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US-09-938-842A-805

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### ALIGNMENTS

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298 GTCGAACCACACATTAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAAT 357
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Sequence 1648, Application US/09880107
Fatent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Ocklef, Uwe
TILLE OF INVENTION Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-14
FRIOR SPELICATION NUMBER: US 60/237,054
FRIOR PRICE PARENTING DATE: 2000-10-02
SOFTWARE PARENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D31815 US-09-880-107-1648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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2378, Ap 1, Appli

Sequence Sequence Sequence

US-10-123-155-144 US-09-974-300-2378 US-10-071-179-1

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434 CTGATAAAAAGGTAAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAACAACCGGAAGTGTTACTGG 733
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233 GTTGATAAAACAACCTCATGCTGCTTCGGAGGGAAGGATTACTCTGAAATGTACGTGACC 292
                                                                   | || || AGGA-----CAAATCCCAGATGGATGTGTATTGATGCTGAGGGAAGGTCTGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 GTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAAAGAAGAAGAGTAGACGAGTACG
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                                            811 TCTGCTGGTCTTCAGCTTGACGACAGTTCTTTNGACAAAAGTTTAGTTAATGGGCACGTC
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43.6; DB 12;
Pred. No. 0.035;
0; Mismatches 179;
                                                                                                                                                 871 TACAGAGTAACAGGTTTAGGCGTCAAAGG 899
                                                                                                                                                                                                                                                                 Sequence 15653, Application US/09918995; Publication No. US20030073623A1; GENERAL INFORMATION:
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US-09-960-352-8453
Sequence 8453, Application US/09960352
Patent No. US2002013713941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-15653
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Matches 180; Conserve
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LENGTH: 471
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: MUSCHER AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCHER AND FAT DEPOSITION
TITLE OF INVENTION: MUSCHER AND FAT DEPOSITION
TITLE OF ILLING DATE: 16511.006/37-21(10299)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILE REPRESSION: 15112
CURRENT FILE CONTINUED DATE: 2001-09-24
SEQ ID NO 5: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGGTCTTTTGAGGCAACCTGAAGCTGGTGGAATTTCAAGATAACTGGTCTGGGGGTC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGTGATCCGTTTGGATCCTGAGACAGGGAAA---AGACTCCAAACTGTGAAGTTGCCT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 TITGGAGGGAAGAATTACTCTGAAATGTATGTGGCCTGCGCCCGGGATGGGATGGACCCC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                          894
                                                                                                                                                                                                                                                                                                                                                          715 CAACCGGAAGTGTTACTGGATACCGTAAAATACCAGATCCTCAGGTCACCTCTGTAGCA 774
                                                                                            GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA 534
                                                                                                                                                                         AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA 594
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                                                                                                                                                                                                                                                                                                                                     GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAAATCAGTACCCAA 714
            AGTTTATATCATTTAGGGGCTGATAAAAGGTAAAAATGCACGAGAGCAACATAGCTATA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 CGAATTATTAAAATCAGTACCCAACAACGGAAGTGTTACTGGATACCGTAAAAATACCA
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Pred. No. 0.025;
0; Mismatches 131; Indels
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US-09-960-352-6109
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Matches 135; Conservative
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ORGANISM:
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Best Local 9
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3100 GAAAATCTAAACAATACCCAATATATAATTAACACTCAATAAATATTTTAAATATATAT 3041
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    GATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAGAGAAAACTTTTCATAAATAT 126
                                                                                                                         Sequence 116286, Application US/10027632
GENERAL INFORMATION:
APPLICANT: wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-03.29
PRIOR FILING DATE: 2000-03.29
PRIOR FILING DATE: 2000-02.24
PRIOR FILING DATE: 2000-02.24
PRIOR FILING DATE: 1999-10.23
PRIOR FILING DATE: 1999-10.28
PRIOR FILING DATE: 1999-09.28
PRIOR FILING DATE: 1999-09.08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASLESEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: FASLESEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: FASLESEQ FOR WINDOWS VERSION 4.0
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PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PLICHG DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PLICHG DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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Best Local Similarity
Matches 63; Conserv
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US-10-027-632-11628
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       APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan APPLICANT: Mathialagan, Nagappan TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352. CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB34-030-Q1-E1-A8
US-09-960-352-8453
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Pred. No. 5.2;
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DE 10019078.8
DE 10019173.8
DE 10035259.7
DE 10043826.1
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2000-04-06
2000-04-07
2000-06-30
Wesley C
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Best Local Similarity 51.1'
Matches 118; Conservative
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SEQ ID NO 209
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Best Local Similarity
Matches 68; Conserv
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627 ATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
                 738 ATTAGGATTTCAAATCAATATAGATTCAGGAATGAAATTTGATATACCAGAAGTAGGTGG 797
                                                                                                                                  798 AGGTACAGATGAAATAAAAACACAACTAAATGAAGAATTAAAAATAGAATATGTCATGA 857
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45.5%; Pred. No. 10;
live 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: POLITAR, MICHAEL R.
APPLICANT: Cardineau, Guy A.
APPLICANT: Schwab, George E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Einstad Lee, Stacey
APPLICANT: Burmeister, Paula
APPLICANT: Dojlilo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA-703C2D1
CURRENT APPLICATION NUMBER: US,10/099,278
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OTHER INFORMATION: Undetermined nucleotide.
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OTHER INFORMATION: Undetermined nucleotide.
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OTHER INFORMATION: Undetermined nucleotide.
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OTHER INFORMATION: Undetermined nucleotide
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OTHER INFORMATION: Undetermined nucleotide
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PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: US 09/378,088
PRIOR APPLICATION NUMBER: US 08/633,993
PRIOR FILING DATE: 1996-04-19
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
NUMBER: OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/10099278 Publication No. US20030106093A1
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Knuth, Mark
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LOCATION: (68)..(68)
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LOCATION: (73)..(73)
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Best Local Similarity
Matches 127; Conserv
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APPLICANT: CARdineau, Guy A.
APPLICANT: Cardineau, Guy A.
APPLICANT: Cardineau, Guy A.
APPLICANT: Schwab, George E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Michaels, Tracy E.
APPLICANT: Dojlilo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA-703CD1
CURRENT APPLICATION NUMBER: US/10/099, 278
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: US 08/633, 993
PRIOR PILING DATE: 1999-04-19
PRIOR PLING DATE: 1996-04-19
PRIOR PLING DATE: 1996-04-19
PRIOR FILING DATE: 1997-04-18
WUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116266
LENGTH: 3290
                                                                                                                                                                                                                                                                                                                                              4.0%; Score 37.2; 59.4%; Pred. No. 6.
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Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bacillus thuringiensis
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Best Local Similarity 45.55
Matches · 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 59.4
Matches 63; Conservative
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US-10-027-632-116286
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                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 292, Application US/10079854
Publication No. US20030054368A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAILOL
CURRENT APPLICATION UNMER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
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                                           Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB 10;
Pred. No. 84;
0; Mismatches 93;
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                         ACAGCGAATTATTAAAATCAGTACCCAACAACCGGAAGT
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Pred. No. 84;
0; Mismatches
                                                                                                                                                            ; Sequence 292, Application US/09764878; Patent No. US20020090615A1; GENERAL INFORMATION:
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Best Local Similarity 49.5%;
Matches 91; Conservative (
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 49.5°
Matches 91; Conservative
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CORGANISM: Homo sapiens
US-09-764-878-292
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LENGTH: 32038
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AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA 506
                                         764
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                                     705 AAAATATCAATATTGGCAACGAGCAGTAGGAAGTAATGTAGCTTTACGTCCACATGAAAA
                                                                             507 GAAAATGTATTATTTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTC
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APPLICANT: DOJILLO, JOANNA
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA-703CD1
CURRENT APPLICATION NUMBER: US/10/099,278
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 09/378,088
PRIOR APPLICATION NUMBER: US 08/633,993
PRIOR APPLICATION NUMBER: US 08/83,993
PRIOR PILING DATE: 1996-04-19
PRIOR FILING DATE: 1996-04-18
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN VERSION 3.1
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45.5%; Pred. No. 13
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Finstad Lee, Stacey
Burmeister, Paula
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Matches 127; Conservative
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642 AACAATIGAIGAGGAGGGIAATITAIGGGIIGCCGTITICCAAGGACAGGGAATIATIAA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 AACGCTTATTGGCGTGGGGGAATTTGGGGACCCTTTCTCCCATTACAATTTTATCAAAAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702 AATCAGTACCCAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGT 761
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                                                                                                            Sequence 2378, Application US/09974300
Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Mathods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT PELLCATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-3-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 2378
LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 48.9%; Pred. No. 14;
Matches 93; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2378
398 GPKPVWGLPQLCRA 411
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Search completed: August 1, 2003, 14:30:57 Job time: 279 secs

Perfect score: Sequence: Scoring table:

OM protein

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Searched:

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Human NOV5e protei
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Drosophila melanog
Sequence gl/32818
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Neisseria meningit
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Z. mobilis aldonol
Staphylococcus epi
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AAB99723
AAG07424
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AAG07422
AAY74581
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281
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N-PSDB; AAF86444.
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Mouse SMP30 SEQ ID
Rat regucalcin, a
Human ageing marke
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Drosophila melanog
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1615
1 MGPVVEKIAELGKYTVGEGP......HVYRVTGLGVKGFAGVKVKL 308
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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ABB06339
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Score

Result

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                                        The present sequence is a firefly protein which regenerates luciferin busing oxyluciferin and D-cysteine. This protein can be used for regeneration of luciferin, a substrate for luciferase, used for ATP (adenosine triphosphate) assays in both medical and food hygiene areas.
                                                                                                                                                                                                                                                                                                                                                                                                                              Luciferin regenerating protein; luciferen; oxyluciferin; luminescence;
                                                                                                                                 1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
                                                                                                                                          VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQP
                                                                                                                  Gaps
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regenerating protein and gene encoding it useful for \mbox{\sc local} no cyclociferin and D-cysteine
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Pred. No. 8.4e-153;
; Mismatches 0;
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                          Claim 7; Page 16-17; 21pp; Japanese
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100.0%;
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           regenerating
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                                                                                                           Local Simi
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                                                                                          The present sequence represents a protein capable of regenerating luciferin. The protein can especially regenerate luciferen from oxyluciferin. The protein can be added to the luciferin-luciferase reaction system to sustain luminescence and reduce the amounts used. The polynuclochide sequence is useful for producing recombinant transformants, which are useful for the production of proteins useful in assaying ATP in medical sciences and food hygiene.
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
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                                          Claim 1; Page 18-19; 23pp; Japanese
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recombinant DNAs and transformants
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Best Local Similarity 56.6
Matches 176; Conservative
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N-PSDB; ABL49712.
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| WAGTLYSKFDIEKQGPNTGTLYSL-SNKQLRKHISNIFLSNGLAWNKDSKKFYFIDSNKR 179
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                 Luciola lateralis-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, useful for producing recombinant DNAs and transformants to give proteins useful in
                                                                                                                                                              The present sequence represents a protein capable of regenerating luciferin, which is isolated from Luciola lateralis (Japanese firefly). The gene encoding the protein capable of regenerating luciferin can be used for producing recombinant DNAs and transformants, which can be used for the production of proteins useful in assaying adenosine triphosphate (ATP) in medical sciences and food hygiene. The protein can be added to the luciferin-luciferase reaction system to sustain luminescence and reduce their amounts used.
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                                                                                                                        Claim 1; Page 18-19; 23pp; Japanese
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                                                                                   assaying adenosine triphosphate
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11-JUL-2000; 2000US-0614150.
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Matches 163; Conservative
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                                                                                                                                           olated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical frugs. The invention in higher euckaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGIT6 ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 303;
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Best Local Similarity 40.7
Matches 121; Conservative
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Adams M,
                                                     WPI; 2001-656860/75
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Venter JC,
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Best Local Similarity
Matches 118; Conserv
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                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                           74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
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                                                                                                                                                                                                           insecticides, therapoutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                             Disclosure; SEQ ID NO 2442; 21pp + Sequence Listing; English.
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Pred. No. 2.3e-46;
8; Mismatches 115;
                                              Myers
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                                                                                                                                                                                                                                                                                                                                            48;
                                              PWD,
                                                                                                                                                                                                                                                                                                                        34.18;
 11-JUL-2000; 2000US-0614150
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                                                                                               New isolated nucleic acid
genes from Drosophila and
interactions
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Best Local Similarity 39.2'
Matches 118; Conservative
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                                             Adams M,
                                                                 2001-656860/75.
                        (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                    303 AA;
                                                                             N-PSDB; ABL02653
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                                              Venter JC,
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74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                          Myers
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                                                                                                                                          PWD,
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39.2%;
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2000US-191637P.
2000US-0614150.
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                                                                                                                                          Adams M,
                                                                                                                                                                                                  WPI; 2001-656860/75
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us-10-089-986-2.rag

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Mus musculus
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                                                                                                                                    cytostatic.
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                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 26868; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Drosophila melanogaster polypeptide SEQ ID NO 26868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 550; DB 22;
Pred. No. 2.3e-46;
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                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
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39.2%;
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                                                              Drosophila melanogaster
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(ABB57737-ABB72072).
                                                                                                                                                                                                                                           Adams M,
                                                                                                                                                                                                                                                                     2001-656860/75.
                                                                                                                                                                                                                (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                  N-PSDB; ABL10795
                                                                                         WO200171042-A2.
                                       pharmaceutical
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                                                                                                                                                                                       11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                       interactions
                                                                                                                                                                          23-MAR-2000;
                         Drosophila;
                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118;
                                                                                                                                                                                                                                           Venter JC,
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The invention relates to a senescence marker protein 30 (SMP30) non-human animal having a defect in the SMP30 function. The animals are useful for producing antibody, evaluating its biological function, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during development of drug and cosmetics including for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-human animals with defective senescence marker protein 30 function, useful for producing antibody, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during
                                                                                                                                                                                                                   marker protein 30; cancer; aging; senescence; SMP30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 YRCGESPVWEEASQSLLFVDIPSKIICRWDTVSNQVQRVAVDAPVSSV--ALRQLGGYVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 36-37; 44pp; Japanese.
ABB83787 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-JP09243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2000; 2000JP-0322234
                                                                                                           (first entry)
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                                                                                                                                                              Mouse SMP30 SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kasahara
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nes 112; Conserv
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KASAHARA N
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(first entry)

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SMP30; senility marker protein; monoclonal antibody; detection.
     03-JAN-1996
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                                        SMP30;
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                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                             123 APAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                  14 YRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALRQSGGYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                   74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                A rat liver cDNA clone coding for a calcium binding protein of mol. wt. 33388 was isolated and sequenced (AAQ87295). The protein was designated "regucalcin" (AAR75416).
                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                        DNA encoding regucalcin - useful for the recombinant production regucalcin, a calcium binding protein
                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                   Length 299;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                 .5; DB 16;
8e-37;
                                                                                                                                                                                                                                                                                                                                                                                 121;
                                                                                                                    'note= "corresponds to CAA codon"
                                                                                                                                     /note= "corresponds to GAC codon"
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 8e-3
                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 454.5; 37.5%; Pred. No. 8e-
                                                   Rat regucalcin, a calcium binding protein
                                                                    rat.
                                                                   Calcium binding protein; regucalcin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR74219 standard; Protein; 299 AA.
                                                                                              Location/Qualifiers
95
¥
                                                                                                                                                                                                                      (DAII-) DAIICHI KAKAGU YAKUHIN KK.
                                                                                                                                                                                                                                                                                                  Claim 1; Page 5-6; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                  41;
standard; Protein; 299
                                                                                                                                                                                      93JP-0279349
                                                                                                                                                                                                       93JP-0279349
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 37.5
nes 111; Conservative
                                                                                                                                                                                                                                               WPI; 1995-211628/28.
N-PSDB; AAQ87295.
                                                                                                                                                                                                                              YAMAGUCHI M
                                                                                                                                                                                                                                                                                                                                                   299 AA;
                                                                                                                             Misc-difference
                                                                                                           Misc-difference
                                                                                    Rattus rattus
                                                                                                                                                      JP07123985-A
                                                                                                                                                                                                       39-NOV-1993;
                                  31-JAN-1996
                                                                                                                                                                                      39-NOV-1993;
                                                                                                                                                                      16-MAY-1995
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR74219;
AAR75416
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                 AAR75416;
                                                                                                                                                                                                                               (YAMA/)
                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
AAR74219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXB
 qq
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70 REVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ90035 is the SMP30 gene. It encodes the human ageing marker protein, SMP30 (AAR74219). Human SMP30 is found in human organs, tissues, blood, urine and cerebrospinal fluid. The blood concentration of SMP30 is known to increase with renal and hepatic deficiencies and to decrease with age. It is therefore useful in the monitoring of renal or hepatic deficiencies and for the monitoring of the development of the liver and kidneys in newborn babies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GESPVWEEVSNSLLFVD-----IPAKKVCRWDSFTKOVQRVTMDAPVSSVALROSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide for detecting human ageing marker protein {\rm SMP30} for monitoring liver and kidney development in new-born babies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.8%; Score 448.5; DB 16; Length 36.9%; Pred. No. 3.2e-36; Live 42; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                     protein; ageing; organ development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              senility marker protein, hSMP30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 7-8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
  Human ageing marker protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW14475 standard; peptide;
                                                                                                                                                                                                                                                                                     93JP-0265681
                                                                                                                                                                                                                                                                                                                                       93JP-0265681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-175363/23
                                                                                                                                                                                                                                                                                                                                                                                               (FJRE ) FUJI REBIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ90035
                                                                                                                                                                                                                                                                                     29-SEP-1993;
                                                           marker
                                                                                                                   Homo sapiens
                                                                                                                                                                        JP07097399-A
                                                                                                                                                                                                                                                                                                                                          29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1997
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule: and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYDASTLSISNORPLFTFEKHEVPGYPDGOTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%; Score 448.5; DB 20; Length 36.9%; Pred. No. 3.2e-36; ive 42; Mismatches 113; Indels
                                                                                                                                                                                              O'Hare M, Obata Y, Old LJ;
Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 775-776; 787pp; English
                                                                                                                                                        INST CANCER RES
            98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11651 standard; Protein;
                                                                                                                                                                                              Gure A,
Sahin U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110; Conservative
                                                                                                                                                                                                                                                                           WPI; 1999-132448/11.
N-PSDB; AAX40196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AA;
                                                                                                                                                                                                Gout I,
                                                                                                                                                                                                                 Pfreundschuh M,
                                                                                                                                                        (LUDW-) LUDWIG
                                                                                            10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ung cancer.
                                   17-JUL-1997
10-OCT-1997
                                                                         10-0CT-1997
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                                                                                                                                                                                                                                        Tureci O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of human senility marker protein (hSMP30) which has a molecular weight of 30 kDa. Monoclonal antibodies recognising hSMP30 are claimed and can be used in a method for detection of the hSMP30 protein in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYVATIGTKFCALNWKEQSAV----VLATVDNDKKNNRFNDGKVDPAGRYFAGTWAEE- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 QTVKLPVDKTTSCCFGGKNYSEMYVTCARDGMDPEGLLRQPEAGGIFKITGLGVKGIA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 DTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GESPVWEEVSNSLLFVD-----IPAKKVCRWDSFTKQVQRVTWDAPVSSVALRQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYDASTLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG----SPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                            Anti-human senility marker protein monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 448.5; DB 18 36.9%; Pred. No. 3.2e-36;
                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 6-7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senescence marker protein SMP30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY06995 standard; Protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US14679.
                                                                                                                                 95JP-0149791
                                                                                                                                                                       95JP-0149791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                               (FJRE ) FUJI REBIO KK.
                                                                                                                                                                                                                                                                                                                   detection of protein
                                                                                                                                                                                                                                                    WPI; 1997-073109/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998;
              Homo sapiens
                                                  JP08319298-A
                                                                                                                                                                       25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9904265-A2
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                                                                                         03-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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180 -GLPTGMPTVHIDGRGKDGGIDGAVCDAEGGLWNARWGVGAVDHYDRTGQHLAR----- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0107387.
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burr TJ, Herlache TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-376567/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA61508.
                                                                                                                                                                                  285
                                                                                                                                           KG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200028056-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36-NOV-1998;
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_ 55
                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2000.
                                                                                                                                                                                                                                                                                                                           AAB11650;
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                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAB11630-B11688 represent proteins from Adrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (AAA61501-A61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development of non-host plants by causing a rapid hypersensitive response that connon-host plants of and killing of the pathogen. On grape plants, the control of plant cells and induction of pathogen resistance. A. vitis elicitor induces a restricted necrosis of tissues, resulting in the elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacterial or viruses; and to enhance growth, e.g., to increase the last or browide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve mutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor content. We allow control of previously untreatable diseases; provide them, may allow control of previously untreatable diseases; provide expense the need for biological control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 SLEREIAILTWDGV---SAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVF------QGQRIIKISTQQP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 VGEGPHWDHETQTLYFVDTVEKTF--HKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAEROM-LATEOGIFIRTIASGELTLLTALEPERPGNRSNDGRVHPCGALWIGTM----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGEGPTYDVARDTAWWFDILGKGLIEHRFATGE------TIRHDLPMMAS-ALATI
                                      Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer;

    A. vitis hypersensitive response elicitor protein, SEQ ID NO:29.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 238; DB 21; Length 293; 26.5%; Pred. No. 3.4e-15; ive 46; Mismatches 126; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 104-105; 157pp; English.
                                                                               stress resistance; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                        Ï
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                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                    98US-0107387.
                                                                                                                                                                                                                                              99WO-US26079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a hypersensitive response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or polluting chemicals.
                                                                                                                      Agrobacterium vitis.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-376567/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA61508
                                                                                                                                                              WO200028056-A2.
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Sequences Ambition Legiblesent process. It now Agrical Sequences Ambition Sequences Ambition February 1971.

Which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (AAA61501-A6154) encoding the A vitts HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development of non-host plants by causing a rapid hypersensitive response that in non-host plants by causing a rapid hypersensitive response that carelly a nating-off and killing of the pathogen. On grape plants, the control investing and induction of pathogen resistance. A vitis elicitor induces a restricted necrosis of tissues, resulting in the elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlact germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A, vitis HR elicitor proteins. Use of A, vitis HR elicitor proteins, and allow control of previously untreatable diseases; provide them, may allow control of previously untreatable diseases; provide systemic treatment; and eliminate the need for biological control agents or polluting chemicals.
                                                                       New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of
241 EVLLDTVKIPDPQVTSVAFGGPNLDELHVTSA--GLQLDDSSLDKSLVNGHVYRVTGLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAB11630-B11688 represent proteins from Agrobacterium vitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. vitis hypersensitive response elicitor protein, SEQ ID NO:28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11650 standard; Protein; 340 AA.
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130

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190
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                                                                                                                                                                                                                                                                       LSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVF-------QGQRIIKISTQQP 240
                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopolesis regulation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipboriatic; antidiabetic; cytostatic; nockropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                         LPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAST
                                                                                                                                                                                                                                EVLLDTVKIPDPQVTSVAFGGPNLDELHVTSA--GLQLDDSSLDKSLVNGHVYRVTGLGV
                                                                                          VGEGPHWDHETQTLYFVDTVEKTF - - HKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                  SLEREIAILTWDGV---SAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAG
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                                                               Gaps
                                                             50;
                                 Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RNA polymerase-like ORF1018 protein, SEQ ID NO:2036.
                                                             Indels
                              ; Score 238; DB 21;
; Pred. No. 4.2e-15;
46; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP32045 standard; Protein; 107 AA.
                              14.7%;
26.5%;
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                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-106200/14.
N-PSDB; ABN76071.
                                          Similarity
340 AA;
                                                                                                                                                                                                                                                                                                                                                                                           KG 300
                                                                                                                                                                                                                                                                                                                                                                                                                          KG 332
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                                                            80;
                            Query Match
Best Local S
Matches 80
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Seguence
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designated ORF (open reading frame) 1-4534, and sequences ABN75054-
ABN79587 represent CDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORFT-ORF4534 (collectival) referred to as ORFX) proteins, polymcleotides at least 80% identical to the ORFT-ORF4534 (collectival) referred to as ORFX) proteins, polymcleotides at least 80% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polymcleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide carried of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, heamatopoiesis regulation, tissue growth, anglogenesis, activity, thrombolytic activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, and antihodies activity, and may also be involved in the determination coll bodily characteristics, fertility and behaviour. ORFX proteins, other proliferative disorders such as psoriasis and benign tumours, and antihogical disorders such as psoriasis and benign tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as disorders of tissue growth and regeneration, storage diseases such as disorders mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 DPLGNLWTGTMAIDAGLPVGPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 KMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 IFYXIDSLSYTVXAFDYDLPTGQISNRRTVXKMEKDE--QIPDGMCIDVEGKL 107
                                                                                                                                                                                                      Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 195.5; DB 2
43.4%; Pred. No. 1.3e-11;
iive 9; Mismatches 44
                                                                                                                                               Claim 10; Page 773; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 43.4 Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA;
                                                                                        transplantation
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Search completed: August 1, 2003, 14:32:07

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Job time

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- 2003 C
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Copyright (c) 1993
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OM protein - protein search, using sw model

Run on:

August 1, 2003, 14:31:08; Search time 37 Seconds (without alignments) 800.254 Million cell updates/sec

Title: Perfect score:

US-10-089-986-2 1615 1 MGPVVEKIAELGKYTVGEGP.......HVYRVTGLGVKGFAGVKVKL 308 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 su

Database :

summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
3: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	anterior fat body	fat		senescence marker			hypothetical prote	RNA polymerase hom	requealein homolog	Smp-30/Cgrl family			probable requcalci	calcium-binding pr	senescence marker	calcium-binding pr	probable calcium-b	calcium-binding pr	requcalcin (AB0379	conserved hypothet	gluconolactonase (	qluconolactonase p	probable gluconola	probable qluconola	probable gluconola	gluconolactonase (	gluconolactonase [	gluconolactonase,	
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SUMMARIES																														
SUMM	ID	JC7250	JC7249	S72173	534588	860035	E95309	AI3216	A70047	B90445	A87351	A87473	G90485	D95265	AB3071	G98215	AH2662	G97444	AF3043	F98242	AH0832	AG3501	AH3051	D98234	C95896	G95274	S28218	B87401	G87512	
	DB	. 7	7	7	7	-	7	7	-	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
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œ	Query Match	34.1	33.3	28.3	28.1	27.8	26.2	25.4	23.3	22.6	20.2	19.5	18.1	17.9	16.9	16.9	15.9	15.9	12.8	12.8	12.6	12.5	9.5	9.5	8.7	8.3	7.7	•	7.0	
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	Result No.	1	7	3	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

RESULT 2 JC7249 anterior fat body protein - flesh fly (Sarcophaga peregrina)

303 V 303

qq

Drp35 protein - St protein Y76A2A.2 [	copper-transportin conserved hypothet	Drp35 [imported] - exopolygalacturona	hypothetical prote	mucin-like protein	gluconolactonase p	probable transamin	hypothetical integ	hypothetical prote	mucin-like protein	hemicentin precurs	probable exported	translation elonga
JC7119 B88612	JC5573 G70302	H90077 F83711	S45911	T45775	B82698	A72257	A81057	AH2060	T45776	T43290	AI0438	T07239
77	7	~ ~	7	~	7	~	7	7	7	7	~	7
324 1116	1238 480	324 1376	358	371	338	384	553	743	371	5198	954	409
6.4	6.4 6.3	6:3 6.3	6.2	6.2	6.1	6.1	0.9	9.0	9.0	5.9	5.9	5.9
104 103.5	103.5 102.5	102	100	100	66	86	97.5	97.5	46	96	95.5	94.5
30	33 33	34 35	36	37	38	39	40	41	42.	43	44	45

### ALIGNMENTS

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C, Accession: JC250
R:Nakajima, Y.; Natori, S.
B. Biocham. 127; 901-908, 2000
A;Title: Identification and characterization of an anterior fat body protein in an in A;Reference number: JC249
A;Accession: JC7250
A;Accession: JC7250
A;Molecule type: mRNA
A;Residues: 1-303 < NAX
A;Cross-references: DDBJ:AB036904
C;Comment: This protein, a homolog of the senescence marker protein-30, has its funct C;Genetics:
A;Gene: afp
A;Cross-references: FlyBase:FBgn0030362
C;Superfamily: senescence marker protein-30
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 GPV----TGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Drosophila sp.
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 TLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Gaps
                                                                                                                                                                                                                                                                                                                                                                               Length 303;
                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.1%; Score 550; DB 2; Length 30 Best Local Similarity 39.2%; Pred. No. 6.5e-37; Matches 118; Conservative 48; Mismatches 115; Indels
anterior fat body protein - fruit fly (Drosophila sp.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 T 308
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NyAlternate manes: regucaling to the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT 246
                                                                                                                                                                                                                                                                                                SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                    GPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 QTGQISNRRIVYKMEKDE--QIPDGMCIDAEGKLWVACYNGGRVIRL---DPETGKRLQT 237
                                                                                                                                                                        14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 PRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALRQSGGVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 YIVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                  14 YRCGESPVWEEASQSLLEVDIPSKIICRWDTVSNQVQRVAVDAPVSSV--ALRQLGGYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule Lype: mRNA
A; Residues: 1-147, 'D', 149-299 <FUJ>
A; Cross-references: EMBL: X69021; NID: 957254; PIDN: CAA48786.1; PID: 957255
C; Superfamily: senescence marker protein-30
C; Keywords: calctum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 299;
                                                   Length 299;
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                                                          5;
                                                   28.3%; Score 457.5; DB 2
llarity 37.8%; Pred. No. 1.9e-29;
Conservative 40; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              senescence marker protein SMP-30 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.19
Best Local Similarity 37.59
Matches 111; Conservative
C; Keywords: calcium binding
                                                                                    Best Local Similarity
Matches 112, Conserv
                                                                                                                                                                                                                                                                                                          74
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
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C.Accession: S72173; S72174  
C.Accession: S72173; S72174  
C.Accession: S72173; S72174  
Diochim: Biophys. Acta 1308, 49-57, 1996  
A.Title: Isolation and characterization of genomic and cDNA clones encoding mouse senesc A.Reference number: S72173; MUID:96328264; PMID:8765750
                                                                                                                                                                                                                                                                                                                    A; Experimental source: larval fat body
A; Accession: PC7071
A: Molecule type: protein
A; Residues: 157-168;174-185;186-195 <NA2>
C; Comment: This protein, a homolog of the senescence marker protein-30, has its function
                                                                                                                                                     protein in an insec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NPTTGKVLLE-IKFPCKQITSAAFGGPNLDILYVTTS-----SRFGEPDPAGTTYKVTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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A;Residues: 1-299 <FUU>
A;Cross-references: EMBL:U28937; NID:g1143999; PIDN:AAC52721.1; PID:g1144000
A;Accession: S72174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID:91144337; PIDN:AAD03478.1; PID:91144338
   C;Species: Sarcophaga peregrina
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: JC7249; PC701
R;Nakajima, Y; Natori, S.
J. Blochem. 127, 901-908, 2000
A;Title: Identification and characterization of an anterior fat body protein A;Reference number: JC7249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PLPDSHAEL----GEGPHWDVATONLYYVDINAGKLLRYNYNENKVYKAKIEGEDLAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 33.3%; Score 538; DB 2; Length 30 Local Similarity 39.0%; Pred. No. 6.1e-36; les 122; Conservative 48; Mismatches 123; Indels
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A; Note: age-associated decrease
C; Superfamily: senescence marker protein-30
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C;Superfamily: senescence marker protein-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          senescence marker protein 30 - mouse
                                                                                                                                                                                                                         A;Accession: JC7249
A;Molecule type: mRNA
A;Residues: 1-306 (ANAX>
A;Cross-references: DDBJ:AB036903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA
A Residues: 1-54 < PUW>
A Cross-references: EMBL: U32170;
A; Experimental source: liver
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || ||: |::|
LGAKGYPMTKIQL 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S72173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-560 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                               A; Gene: SMa0717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Accession: E95309
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Kaating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9889, 2001
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-569 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence 25, 1995
A; Fujite, T.; Mandel, J.L.; Shirasawa, T.; Hino, O.; Shirai, T.; Maruyama, N.
Biochim. Biophys. Acta 1263, 249-252, 1995
A; Title: Isolation of CDNA clone encoding human homologue of senescence marker protein-3 A; Reference number: 152491; MUID: 9604897; PMID: 7548213
A; Reference number: 152491; MUID: 9604897; PMID: 7548213
A; Residues: 1-299 <FUJ>A; Residues: 1-299 <FUJ>A; Cross-references: EMBL: D31815; NID: 91072311; PIDN: BAA06602.1; PID: 91072312
C; Genetics: A; Genetics: A; Cross-references: A; Cross-reference
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8
                                                                   246
                                                                                                ---TAPAVLERHQGALYSLFPDHHVKKYFDQVDISNGLDWSLDHKIFYYIDSLSYSVDAF 178
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   APAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL 182
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N'Alternate names: regucalioin
C.Species: Homo sapiens (man)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                       VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKY---TFCKVDKLVSFIIPLAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 448.5; DB 1;
; Pred. No. 1e-28;
42; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references. uzz.z. A; Map position: Xp11.3; Xp11.2 C; Superfamily: senescence marker protein-30 C; Keywords: calcium binding
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36.9%;
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Best Local Similarity 36.99
Matches 110; Conservative
   123
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Species: Agrobacterium timefaciens
C; Decies: Agrobacterium timefaciens
C; Date: 11.3an-2002 #sequence_revision 11.3an-2002 #text_change 11.3an-2002
R; Mocd, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
A;Cross-references: GB:AE006469; PIDN:AAK65039.1; PID:g14523470; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandeabol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizoblum meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Atu5464 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 EREIAILTWDGVS------AAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 EREIAILTWDGV---SAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 NECLIVASQDGVEHFDFDRGDFNPFAEP-----EPGLPENRLNDAKVDPSGRLWVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 IGEAPVWVEREKRLYWVDILHPAVHRFDPVTGKNESCNVAKLVSAVLP-----TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVL
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regucalcin homolog [imported] - Sulfolobus solfataricus
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Matches 9
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RNA polymerase homolog yvrE - Bacillus subtilis
C;Species: Species
C;Species: Species
C;Species: Species
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, K.; Lapidus, A.; Lardinois,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Schosto, T.; Scanlon,
A; Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Willy A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Reference number: A65580; WID:98044033; PMID:9384377
A; Rocession: A70047
A; Reterence number: A6580; WID:98044033; PMID:9384377
A; Rocession: A7004
A; Reterence number: Gravagaion: Gravagaion: Chriyama, A; Reterence number: Gravagaion: A70047
A; Reterence number: Gravagaion: A
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A:Experimental source: strain 168
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                                                                                                                                                                                                                                  28
VGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLS 192
                                                                                                                                                                                                                                                                                                                                          249 IPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYR----VTGLGVKGFAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 ER----EIAILTWDG---VSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAID
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                                                                                                                                         ----TGALYRINANGASERKEGGIIVSNGLGWSPDGRTFYFYDTVPGLIHAYDCDPATGA
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31.5%; Pred. No. 7.2e-23;
iive 52; Mismatches 105;
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85; Conservative
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Matches 8
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C; Species: Sulfolobus solfataricus
C; Date: 24-may-2001 #sequence_revision 24-may-2001 #text_change 15-Jun-2001
C; Date: 24-may-2001 #sequence_revision 24-may-2001 #text_change 15-Jun-2001
C; Date: 20-may 1: Joint 1: Joint
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Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Ocher-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
Cispeciesion: A87351
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Heit, D.H.; Ko
D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87351
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A; Residues: 1-289 <STO>
A; Cross-references: GB:AE005673; NID:g13422069; PIDN:AAK22805.1; GSPDB:GN00148
C; Genetics:
A; Gene: CC0820
C; Superfamily: senescence marker protein-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 TGKKLFE-IKVPATYVTSVTFGTQELDQLFITTAGKSQDP-----LAGKTF-TTKANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 KYTVGEGPHWDHETQTLYFVD------TVEKTFHKYVPSQKKYTFCKVD--KLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFIIPLAGSPGREVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLG
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No. 3.1e-19;
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RGLONFRFKI 284
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Local Similarity
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Best L
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probable requeatein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid psy c;Species: Sinorhizobium meliloti (c;Species: Sinorhizobium meliloti) (c;Species: Sinorhizobi
                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                  conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKLVSFIIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIK - - - - - NNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 NDGKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.1%; Score 292; DB 2; 30.1%; Pred. No. 4.3e-16; tive 50; Mismatches 101;
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Matches 85; Conserv
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C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87473
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laulo, M.T.; DeBoy, R.T.; DodSon, R.T.; DodSon, R.T.; Shapiro, L.; Venter, J.C.; Fraser, J. C. M.
Froc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
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     10;
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                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                          72 VVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGL 131
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                                                                         SISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD
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                                             13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQ-KKYTFCKVDKLVSFIIPLAGSPGRF
                                                                                                                                                                                                                                          132 PVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSL
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                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.5%; Score 315; DB 2; L 30.9%; Pred. No. 6.2e-18; iive 51; Mismatches 115;
     Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CC1805
C;Superfamily: senescence marker protein-30
47;
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Best Local Similarity 30.97
Matches 93; Conservative
     Conservative
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94;
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STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPE-VLLDTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: AGR_L_1336
A;Map position: linear chromosome
C;Superfamily: senescence marker protein-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: August 1, 2003, 14:35:00
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                                                                                  KIPDPQVTSVAFGGPNLDELHVTS 271
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31.1%;
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Best Local Similarity 31.1%
Matches 82; Conservative
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Ob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB3071
                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-293 <KUR>
A; Cross-references: GB: AE008689; PIDN: AAL44984.1; PID: 917742642; GSPDB: GN00187
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 RFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDA 129
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                                                                                                                                                                                                                                                                                                                                                                DYDASTLSISNQRPLFT-FEKHEVPGYPDGQTIDEEGNLW-----VAVFQGQRIIK 234
                                                                                                                                                                                                                                                                                                                                                                                       235 ISTQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVT 294
                                                                                                                                                                                                                    FVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMA--ID 128
                                                                                                                                                                                                                                             13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAG--SPGR 70
                                                                                                                                                                      21 VGESPTWDERTGDLWFVDILAPAIFCLSPS------GRLQRFDMPAQIGCLGLCQSN
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                                                                    Length 311;
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                                                                                                         Indels
                                                                    17.9%; Score 288.5; DB 2; 28.1%; Pred. No. 9.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.18; Pred. No. 1.6e-14;
Matches 82; Conservative 39; Mismatches 113
                                                                                                         47; Mismatches
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A;Gene: SMa0060
A;Genome: plasmid
C;Superfamily: senescence marker protein-30
                                                                                                             Conservative
                                                                                        Best_Local Similarity
Matches 85; Conserv
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GVG 289
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Series cence marker protein-30 (AB03336B) [imported] - Agrobacterium tumefaciens (strail c) Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Feb-2002
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 15-Feb-2002
C; Accession: G98215
B; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-232B, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-322 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89249.1; PID:g15159075; GSPDB:GN00170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPE-VLLDTV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 OTGRLGPAKRLHDFQPDE--GRPDGAATDSEGCYWSAGVQAGRLNRFT---PDGELFEIY 267
16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPL-AGSPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 273; DB 2;
Pred. No. 1.8e-14;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 1, 2003, 14:25:59; Search time 22 Seconds (without alignments) 580.669 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-089-986-2 1615 1 MGPVVEKIAELGKYTVGEGP..........HVYRVTGLGVKGFAGVKVKL 308

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

Minimum DB seq length.: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMARIES		
Result		Query					•
No.	Score	Match	Length	DB	OI	Description	
1	459	ω	299	П	SM30_RABIT		oryctolagus
7	S	28.3	299	1	SM30_MOUSE	-	musculu
æ	2	28.1	299	٦	SM30_BOVIN	pos	taurus
4	454.5	ω	299	7	SM30_RAT		rattus norv
S	4	7	299	-	SM30_HUMAN		homo sapien
9	391.5	24.2	275	٦	Y31K_SULAC		lobus
7	376	23.3	292	П	YVRE_BACSU	034940 bacillus	ns sn
80	235	4.	340	П	CGR1_CANAL		ത
б	124.5		320	٦	GNL_ZYMMO	Q01578 zymomonas	onas m
10	100	٠	358	-	YBQ3_YEAST		saccharomyc
11	94.5		409	_	EFTU_CHLVU	P56292 chlorella	ellav
12	94		401	٦	PGK_HALVA		rcula
13	92.5	٠	4351	П	FAT2_RAT		rattus norv
14	92		4349	Н	FAT2_HUMAN		homo sapien
15	91.5	•	242	1	RL1_STRVG		streptomyce
16	91.5	٠	663	П	ABA2_NICPL		iana p
17	91	5.6	366	7	XYNA_BACHD	P07528 bacillus	lus ha
18	91	•	268	7	FTS1_BUCAP	085297 buchnera	era ap
19	90.5	٠	242	П	RL1_STRSQ		streptomyce
20	90.5	•	539	1	CH61_BRAJA		bradyrhizob
21	90.5	٠	545	П	CH63_BRAJA		bradyrhizob
22	89.5	•	387	П	XYLA_THETH		is the
23	88		892	-	LDL2_XENLA		ıs lae
24	88.5	•	294	Н	OCCT_RHIME		oium m
25	88.5	٠	431	Н	SPAL_SALTY		nella
56	88	5.4	922	~	DPO1_RICFE	Q9raa9 rickettsia	ttsia
27	87.5	5.4	242	-	RL1_STRAU		streptomyce
28	87.5	5.4	862	Н	LOX1_HORVU		ım vul
29	87	5.4	745	П	RNR_BUCAI	_	era ap
30	87	5.4	1071	1	CARB_BACSU	P25994 bacillus	
31	86.5	5.4	720	Т	VP19_BPAPS	t1s9	bacteriopha
32	98	5.3	405	П	DHMH_METME	-	lophil
33	82	5.3	350	7	RLA0_HALVO	41198	acteri

85 5.3 426 1 CGED BACSU 85 5.3 634 1 FLIC_SALMO 85 5.3 634 1 FLIC_SALMO 85 5.3 992 1 YV93_MYCTU 84.5 5.2 11 1 ACLY_HUMAN 84.5 5.2 757 1 AMO_ECOLI 84.5 5.2 139 1 HMML_MYGGE 84.5 5.2 139 1 HMML_MYGGE 84.5 5.2 139 1 LRP2_RAT 83.5 5.2 77 1 LRP2_RAT 83.5 5.2 77 1 LRP2_RAT 83.5 5.2 77 1 LRP2_RAT 83.5 5.2 77 1 LRP2_MAUSE 83.5 7.7 1 TRP2_MAUSE	bacillus su	salmonella	saccharomyc	mycobacteri	homo sapien	drosophila	escherichia	mycoplasma				
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888888 4 4 8 8 8 8 8 8 8 8 8 8 8 8	CGED_BACSU	FLIC_SALMO	UBA2_YEAST	YV93_MYCTU	ACLY_HUMAN	YELL_DROYA	AMO_ECOLI	HMW1_MYCGE	LRP2_RAT	CH60_STAAU	ITB2_MOUSE	COPG_YEAST
888888 88888 8. 4. 4. 4. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8.	Н	Н	<del>, ,</del>	Н	-	Н	H	Н	Н	-	٦	-
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	5.3	5.3	5.3	5.3	5.3	5.2	5.2	5.5	5.2	5.2	5.2	5.2
88888888444444444444444444444444444444	82	82	82	85	85	84.5	84.5	84.5	84	83.5	83.5	83.5
	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

SUL 30_	Query Match Best Local Similarity Matches 114; Conserva	Qy 17 GEGPHWDHETQTLXFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLE 76	QY 77 REIALLTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTWAIDAGLFYGPV 136 1:	Qy 137 TGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL 191 		30L 30L 30Le 30Le 30Le
	Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  NCBL_TaxID=986;  [1] SEQUENCE FROM N.A. TISSUE=Liver; MEDLINE=20351777; PubMed=10891565; MEDLINE=2035445; PaA888079.1; MEDLINE=2035445; PaA88079.1; MEDLINE=2035445; PaA888079.1; MEDLINE=2035445; PaA888079.1; MEDLINE=2035445; PaA888079.1; MEDLINE=2035445; PaA888079.1; MEDLINE=2035445; PaA888079.1; MEDLINE=2035475; PaA888079.1; MEDLINE=2035475; PaA888079.1; MEDLINE=2035475; PaA888079.1; MEDLINE=2035475; PaA888079.1; MEDLINE=2035475; PaA888079.1; MEDLINE=2035476; PaA888079.1; MEDLINE=203	Due Bes Mat	2 Aat Mat	Due 3es 4at	A D D D D D D D D D D D D D D D D D D D	O9TTJ5; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) PGN OP SMR30
USTIND; 15-TUN-2002 (Rel. 41, Created) 15-TUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Senescence marker protein-30 (SMP-30) (Regucalcin)		Due Bes	Saes Mat	Aat Aat	80008	
		2ue 3es	2ue 3es	2ue 3es Mat	RY RX RX	11) TISQUENCE FROM N.A. TISSUE-Liver; MEDLINE-20351777; PubMed-10891565; Misawa H., Yamaguchi M.;
		Due 3es Mat	Que 3es Mat	2ue 3es Mat	# # # B B B B B B B B B B B B B B B B B	
·	SECUENCE AS AA	SEQUENCE 299 AA; 33108 MW; ABF94AD596AUCB8 CKC64; Ouery Match . 28.4%; Score 459; DB 1; Length 299; Best Local Similarity 38.1%; Pred. No. 2.9e-29; Matches 114; Conservative 41; Mismatches 116; Indels 28; Gaps 8	SEQUENCE 299 AA; 31108 MW; ABF94ADD596ADCB8 CKC64;  Duery Match  28.4%; Score 459; DB 1; Length 299;  Bast Local Similarity 38.1%; Pred: No. 2.9e-29;  Matches 114; Conservative 41; Mismatches 116; Indels 28; Gaps 8  17 GECPHWDHETQTLFVDTVEKTFHKYDSQKYTFCKVDKLVSFIIPLAGSPGRFVVSLE 76  1	SEQUENCE 299 AA; SIUB MW; ABF94ADD596ADCBB CKC64;  Duery Match  28.4%; Score 459; DB 1; Length 299;  38.1%; Pred. No. 2.98-29;  4atches 114; Conservative 41; Mismatches 116; Indels 28; Gaps 8  17 GECPHWDHETQTLYFVDTVEKTFHKYVDSQKKYTFCKVDKLYSFIIPLAGSPGRFVVSLE 76  18.	888888888888 <b>≅</b> €	
	17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLE	77 REIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTWAIDAGLPVGPV :	137 TGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL 1111   1   1   1   1   1   1   1   1		Ωy	192 SISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKI 249

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 REIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VLERRQGSLYSLFFDHHVEKYFDQVDISNGLDWSMDHKIFYXIDSLSYSVDAFDYDLQTG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDTVKI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTL 191
                                                                                                                           STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLLDT 246
GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                           17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misawa H., Yamaguchi M.;
"The gene of Ca2+-binding protein regucalcin is highly conserved in vertebrate species.";
Int. J. Mol. Med. 6:191-196(2000).
Int. J. Mol. Med. 6:191-196(2000).
IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE AGED LIVER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                 247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                   238 VKLPVDKTTSCCFGGKDYSEMYVTCARDGLNAEGLLROPDAGNIFKITGLGVKGIA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 454.5; DB 1; Length 299; 38.1%; Pred. No. 6.6e-29; ive 38; Mismatches 119; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC)
RGN OR SMP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 AA; 33308 MW; 4258F7CDB3CCB575 CRC64;
                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20351777; PubMed-10891565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB035446; BAA88080.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-binding.
                                                                                                                                                                                                                                                                                                                                    SM30_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                            134
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                        72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murata T., Yamaguchi M.;

Murata T., Yamaguchi M.;

Muccular cloning of the cDNA coding for regucalcin and its mRNA
expression in mouse liver: the expression is stimulated by calcium
administration.";

Mol. Cell. Biochem. 173:127-133(1997).

IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
CALCIUM SIGNALING IN THE AGED LIVER.

CALCIUM SIGNALING IN THE AGED LIVER.

TISSUE SPECIFICITY: MAINLY PRESENT IN THE LIVER. WEAK EXPRESSION
AS FOUND IN THE BRAIN AND LUNG, NOT FOUND IN THE KIDNEY.

SIGNIFICANITY WITH AGE.

SIGNIFICANITY WITH AGE.

SIGNIFICANITY WITH AGE.

SIGNIFICANITY WITH AGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1
       14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                            PDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG----FAG 303
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujita T., Shirasawa T., Maruyama N.; Isolation and characterization of genomic and cDNA clones encoding mouse senescence marker protein-30 (SWF30)."; Biochim. Biophys. Acta 1308:49-57(1996).
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                         SM30_MOUSE STANDARD; PRT; 299 AA.
064374; Q60944;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAD55EF618311977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.3%; Score 457.5; DB 1; 37.8%; Pred. No. 3.8e-29; iive 40; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-96328264; PubMed-8765750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97422495; PubMed-9278263;
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Calcium-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
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Matches
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EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOUND IN 5-DAY-OLD NEONATES. EXPRESSION INCREASES FROM DAY 7 AND BEACHES A PLATEU AT DAY 10. 3-6.5 MOTH-OLD ADULIES EXPRESS ABOUT A THIRD THE AMOUNT OF NEONATES LEVEL. IN KIDNEY, EXPRESSION INCREASES FROM DAY 21 AND REACHES A MAXIMAL LEVEL AT DAY 35, FEMAINS HIGH UNITL 3 MONTHS OF AGE.

PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimokawa N., Matsuda Y., Yamaguchi M.; "Genomic cloning and chromosomal assignment of rat regucalcin gene."; Mol. Cell. Biochem. 151:157-163(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mech. Ageing Dev. 87:219-229(1996).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMATIC ACTIVITY IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE AGED LIVER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: HEPATOCYTES AND RENAL PROXIMAL TUBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMP30): coordinated
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: IN LIVER, THE FIRST PEAK OF EXPRESSION WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimokawa N., Yamaguchi M.;
"Molecular cloning and sequencing of the cDNA coding for a calcium-
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93041931; Pubmed=1420310;
Fujita T., Shirasawa T., Uchida K., Maruyama N.;
Isolation of Cohn clone encoding rat senescence marker protein-30
(SMP30) and its tissue distribution.; (SMP30) and its Lissue 1132:297-305(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY.

BEDLINE-96386712: PubMed=8794449;

Fujita T., Shirasawa T., Uchida K., Maruyama N.;

Fujita T., Shirasawa T., Uchida K., Maruyama N.;

"Gene regulation of senescence marker protein-30 (SMP30): coordinup-regulation with tissue maturation and gradual down-regulation
                                         PDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG 300
                                                             SM30_RAT STANDARD; PRT; 299 AA.
003336; 063496;
01-0CT-1993 (Rel. 27, Created)
01-0V-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from rat liver.";
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE-Kidney;
MEDLINE-96150990; PubMed-8569761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TISSUE=Liver;
MEDLINE=93351639; PubMed=8348951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding protein regucalcin fro
FEBS Lett. 327:251-255(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 117-299 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           STRAIN-Wistar; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 TIGTKFCALNWE-----DQSVFILAMVDEDKKNNRFNDGKVDPAGRYFAGTMAEE----T 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 APAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDWSLDHKIFYYIDSLSYTVDAFDYDL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                    14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                          14 YRCGESPVWEEASKCLLFVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALRQSGGYVA 71
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-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMATIC ACTIVITY IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF CALCIUM SIGNALING IN THE ADD LIVER.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misawa H., Yamaguchi M.;
"Transcript heterogeneity of the human gene for Ca2+-binding protein
regucalcin.";
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
MEDLINE=9604897; PubMed=7548213;
RUJIta T., Mandel J.L., Shirasawa T., Hino O., Shirai T., Maruyama Fujita T., Mandel J.L., Shirasawa T., Hino O., Shirai T., Maruyama Fisolation of CDNA clone encoding human homologue of senescence marker protein-30 (SMP30) and its location on the X chromosome.";
Blochim. Blophys. Acta 1263:249-252(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                      DB 1; Length 299;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                     N -> D (IN REF. 1).
E3CF6D3FFCAE4E98 CRC64;
                                                                                                                                                                                                                                                              Pred. No. 6.6e-29;
41; Mismatches 121;
                                                                                                                                                                                                                                      Score 454.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                33389 MW;
EMBL; X69021; CAA48786.1; -. EMBL; D38467; BAA07490.1; -. EMBL; D31662; BAA06507.1; -.
                                                                                                                                                                                                                                      28.1%;
                                                                                                                                                                                                                                                                 37.5%;
                                                                                                                                                                                                                                                                    Local Similarity 37.5 nes 111; Conservative
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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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                                                                                            PIR; S27203; S27203
                                                                                                                                                                                299 AA;
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                                                                                                                    Calcium-binding.
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ID SM30_HUMAN
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-:- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY
-:- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RNA POLYMERASE
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01-NOV-1995 (Rel. 32, Last sequence update)
11-JUL-1998 (Rel. 36, Last annotation u
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 299;
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                                                                                                                                                                                                                                                                                                                                                    299 AA; 33253 MW; 95BA1C73B7B77635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 448.5; DB 1;
36.9%; Pred. No. 2e-28;
live 42; Mismatches 113;
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                                                                                                                                                           EMBL; D31815; BAA06602.1; -.
EMBL; AB028125; BAA78693.1; -.
EMBL; AB032064; BAA84082.1; -.
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Best Local Similarity 33.0°
Matches 98; Conservative
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                                                                                                                                                                                                                                                           Genew; HGNC:9989; RGN.
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275 AA; 3
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SEQUENCE FROM N.A.
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SEQUENCE 299 A
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SEQUENCE 27
                                                                                                                                                                                                                                                                                         MIM; 300212;
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Matches 110;
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127 IDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDY 186
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                                                                                                                                                             FVVSLEREIAIL----TWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMA
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----LAGSPGR
                                                           EGPIWAY--NSLYFVDIPKGELHN-LKEDGTHWVVKPPTYVSSLQPTKRGGIIVTAGNGF
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Wipat A., Brignell C.S., Guy J.B., Rose M., Emmerson P.T.,
Harwood C.R.;
EGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yvrE.
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Microbiology 144:1593-1600(1998).
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Q01578;
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Best Local 3
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ER----EIAILTWDG---VSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAID 128
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Viari A., Wambutt.R., Wedler E., Wedler H., Weitzenegger T., Wifers P., Wipat A., Yamamoto H., Yamamoto K., Yasumoto K., Yashida K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
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~hes 105; Indels
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Cho T., Sudoh M., Tanaka T., Nakashima Y.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE CELL GROWTH REGULATION.
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D68A0812FC8D90AB CRC64;
                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33204 MW;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ223978; CAA11732.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.3%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z99120; CAB15310.1; -. EMBL; Z99121; CAB15325.1; -.
                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 31.5 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SubtiList; BG14145; yvrE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell growth protein CGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein;
292 AA; 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGR1_CANAL
P56553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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  g
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                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 -IPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNN------RLNDGKA 114
                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1171:198-200(1992).
-!- FUNCTION: HYDROLYZES THE GLUCONOLACTONE FORMED BY GLUCOSE-FRUCTOSE OXIDOREDUCTASE, AND THAT FORMED IN AEROBIC CONDITIONS BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Periplasmic (Probable).
-:- CAUTION: IT IS POSSIBLE THAT IN SOME CASES MET-40 IS THE INITIATOR IN THIS CASE THE EXPRESSED ENZYME WOULD REMAIN CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                  GKYTVGEGPHWDHETQTLYFVDTVEKTFHKYV-----PSQKKYTFCKVDKLVSFI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPLGNLWTGTMAIDAGLPVG-----PVTGSLYHLGADKKVK------MHESNIAIANGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 DPWGNLWIGVM---NDFPIGAKEGIQPEGKLYRIGFSKESNKLTCDVMIENSL-ISNGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 GNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQVTSVAFG-GPNLDELHVTSAGLQLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 WSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVP----GYPDGQTIDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanagasundaram V., Scopes R.;
"Isolation and characterization of the gene encoding gluconolactonase

    -!- CATALYTIC ACTIVITY: D-glucono-1,5-lactone + H(2)0 = D-gluconate.
    -!- PATHWAY: SECOND STEP IN SORBITOL PATHWAY.
    -!- SUBUNIT: HOMODIMER.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Gluconolactonase precursor (EC 3.1.1.17) (D-glucono-delta-lactone
                                                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                  Length 340;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                              EMBL; AB013716; BAA28176.1; -.
SEQUENCE 340 AA; 38391 MW; 4B1673ED448D1F7A CRC64;
                                                                                                                                                                                                                                                               ch 14.6%; Score 235; DB 1; Le
l Similarity 26.9%; Pred. No. 1.9e-11;
84; Conservative 55; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 36-58.
STRAIN-ATCC 29191 / ZM6;
MEDLINE-93129619; PubMed-1482681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCOSE DEHYDROGENASE PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 26, Created)
(Rel. 26, Last sequ
(Rel. 27, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::: | :: |
302 EKATIDATNLDG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 --SSLDKSLVNG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Zymomonas mobilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Score 100;
                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=IAM C-27 / Tamiya;
MEDLINE=97303241; Pubmed=9159184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_Cterm.
EFTU_D2.
EF_GTPbind.
Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB001684; BAA57886.1; -.
HSSP; P07157; 1AIP.
                                        40295 MW;
                                                                  6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004541; EF-Tu.
                                                                                              52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
PIR; S45911; S45911.
SGD; S0000257; YBR053C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004160;
                         Hypothetical protein. SEQUENCE 358 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005225;
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                   EFTU_CHLVU
                                                                                                                                                   148
                                                                                                                                                                                                                                  213
                                                                    Query Match
Best Local
                                                                                             Matches
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  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                         76 EGPVWVKNGNFLLFSDPPANIMRKWTP------DAGVSIFLKPSGHAEPIPAGOFR 125
                                                                                                                                                                                                                                                                                                                   78 EIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLW---TGTMAIDAGLPVG 134
                                                                                                                                                                                                                                                                                                                                                                        135 PVT------HLG 144
                                                                                                                                                                                                                                                                                                                                                                                                155 PVTRQRSVVDNYKGKRFNSPNDLFFSKSGAVYFTDPPYGLTNLDESDIKEMNYNGVFRLS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 PDGRLDLIEAGLSRPNGLALSPDETKLYVSNSDRASPNIWVYSLDSNGLPTSRTLLRNFR 274
                                                                                                                                                                                                                                                               EGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLER
                                                                                                                                                                                                                                                                                                                                              126 E------PGS-----MKVD
                                                                                                                                                                                                                                                                                                                                                                                                                             145 ADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLF-TFE
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aljinovic G., Pohl T.M.; \mbox{\sc R} "Sequence and analysis of 24 kb on chromosome II of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical 40.3 kDa protein in REG2-YRO2 intergenic region. YBR053C OR YBR053C. Sacubaromyces cerevisiae (Baker's yeast). Saccharomyces cerevisiae (Baker's yeast). Saccharomyceta: Saccharomycetaes; Saccharomycetaes; Saccharomycetaes; Saccharomycetaes.
                                                                                                                                                                                                                                     66
                                                                                                                                                                                                        7.7%; Score 124.5; DB 1; Length 320; 21.8%; Pred. No. 0.0099; Ive 26; Mismatches 83; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Hypothetical 40.3 kDa protein in REG2-YRO2 intergenic region.
                                                                                                                                                                     (MINOR FORM).
                                                                                                                                                      GLUCONOLACTONASE.
GLUCONOLACTONASE (MINOR FG
7552DE348D83564C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reast 11:4/2-4/9(1992).
-!- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
                                                  EMBL, X67189; CAA47637.1; -.
PIR; S28124; S28124.
PIR; S28218; S28218.
InterPro; IPR000033; Ldl_receptor_rep.
SMART; SM00135; LY; 1.
Hydrolase; Serine estrase; Periplasmic; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 AA
     not removed.
    modified and this statement is not removentities requires a license agreement (S) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 K----HEVPGYPDGQTIDEEGNLWVA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | ||| ||::||||: : | 275 KEYFDQGLAGLPDGMNIDKQGNLFAS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95321020; PubMed-7597852;
                                                                                                                                                                                320 AA; 34767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 235922; CAA84996.1; -. EMBL; 246260; CAA86396.1; -.
                                                                                                                                                                                                                        21.8%;
                                                                                                                                                                                                                          Local Similarity 21.8%
Les 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevisiae.";
Yeast 11:475-479(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YBQ3_YEAST
P38235;
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                             Query Match
                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YBQ3_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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                                                                                                                                                                  108 RLNDGKADPLGN-LWTGTMAIDAGLPVGPVTGSLYHLG-ADKKVKMHESNIAIANGLAW- 164
                                                                                                                                                                                                                                                                                                                           GQTI-----DEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD--PQVTSVAFGGPNL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Chlorophyta; Trebouxlophyceae; Chlorellales; Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                   165 SNDLKKMYYIDSGK-----RRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                            Length 358;
                                                                                        73; Indels
0091701F98ED87C9
                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 KDLFVTTANAEINDAVRTNTDKN--GGCIYKI 339
                                                                                                                                                                                                                                                                                                                                                                                                                         265 DELHVTSAGLQLDD---SSLDKSLVNGHVYRV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 AA
                                                                                           41; Mismatches
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HL-----DEKVDDFLLGGI-AGTVPAAAGHPVGYDIDDANLYDEQWEANSEKIESMLED 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIKNNRLNDGKADP--LGNLWTGTMAIDAGLPVG-----PVTGSLYHLGADKKVKM--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AHRSHASLVGFPLVMDAYAGR-VMETEYEANTAIAEKEFDGQVTMVVGGTKATDVIDVMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PIIRESEAVFGEGR--AGMFEDERFSVGTAGVLEAIADT-----DCFSVV
                                                                                                                                                                                                                                                                                                                                                                                                2 GP-VVEKIAELGKYTV------GEGPHWDHETQT-LYFVDTVEKTFHKYVPSQKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                      94 GPQAIHDIADLDSGDVLVLENTRMCDDELPEEDPEVKAQTEFVKTLAGEFDAYINDAYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 TFCKVDKLVSFIIPLAGSPGRFVVSLERE----IAILTWDG---VSAAPTSIEAIVNVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HESNIAIANGLAWSN--------DLKKMYYIDSGKRRVDEYDYDASTLSISNQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 HRDQITLAVDLAYEDENDDRAEQAVDDIDEKRLSYLDVGSETLMEYS------
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last unotation update)
Protocadherin Fat 2 precursor (Multiple epidermal growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 FGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG-----FAGVKV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGD-----TSRAIEMYGMEEDEF---GHVSIAGGAYIRALTRAQLVGVEV 398
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STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINR=98360089; PubMed=9693030;
Makayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O "Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                            5.8%; Score 94; DB 1; Length 401; 22.1%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                     137; Indels
                                                                                                                                                                                                                                                                 ACDD98F8856B490E CRC64;
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-!- SIMILARITY: CONTAINS 33 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4351 AA
                                                                                                                                                                                                                                                                                                                                                   42; Mismatches
                                                                                                                                                                         Pfam; PF00162; PGK; 1.
PRINTS; PR00477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                               Kinase; Glycolysis.
31 AA; 44193 MW; AC
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Rodentia;
                                                                                                            EMBL; L47295; AAB03731.1; -. HSSP; P18912; 1PHP.
                                                                                                                                   HSSP; P18912; 1PHP.
InterPro; IPR001576; PGK.
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 78; Conserv
                                                                                                                                                                                                                                                                 401 AA;
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FAT2 OR MEGF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 LEREIAILTWDGVSAAPTSIEAIVNVE-PHIKNNRLN------DGKADPLGNLWTGTM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AIDAGLPV----GPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 EDOVD-DAELLELLELEIRETLDKYEFPG-----DE----IPIISGSALLALEALTE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 NPETKPGDNKWVDKIYNLMDQVDSYIPTPERETEKPFLMAVEDVFSITGRGTVATGRVER 244
                                                                                                                                                                                                                                                                                                                                                                                                                                  17 TIG---HVDHGKTILTAAITMA------45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GPNL------DELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKIS--TQ
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"Higher-plant chloroplast and cytosolic 3-phosphoglycerate kinases: case of endosymbiotic gene replacement.";
Plant Mol. Biol. 30:65-75(1996).
-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.
-!- PATHWAY: Second phase of glycolysis; second step.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                     Indels 141;
                                                                                                                                                                                                                                                                                                          DB 1; Length 409;
                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 0183143E5E117999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.
NCBI_TaxID=28442;
                                                                                                                              PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; Chloroplast;
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                      5.9%; Score 94.5; DE 19.6%; Pred. No. 3.2; ative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 AA
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PTMTMTS; PR00315; ELONGATNECT.
TIGRPAMS; TIGR00231; Small_GTP; 1.
TIGRFAMS; TIGR00485; EF-TU; 1.
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409 AA; 44911 MW;
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(Rel. 34, Last seq
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85
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81
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P50315:
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SEQUENCE
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CARBOHYD 1175 11 CARBOHYD 1276 12 CARBOHYD 1417 14 CARBOHYD 1998 19 CARBOHYD 2007 2102 CARBOHYD 2105 2102 CARBOHYD 2325 23 CARBOHYD 2368 23 CARBOHYD 2368 23 CARBOHYD 2470 2470 CARBOHYD 2470 2470 CARBOHYD 2470 2470 CARBOHYD 2470 2470 CARBOHYD 3713 3312 CARBOHYD 3713 3312 CARBOHYD 3713 370 CARBOHYD 3718 3875 CARBOHYD 3875 36 CARBOHYD 3876 30 CARBOHYD 3870 370 CARBOHYD 3870 CARBOHY	DT 15-JUN-2002 (Rel. 41, Last annotation upwate)  DE Protocadherin Fat 2 precursor (hFat2) (Multiple epidermal growth  DE factor-like domains 1).  GN FAT2 OR MEGF1 OR CDHF8.
CC centified and this statement is not removed, usage by and for commercial central requires a literase agreement (See http://www.isb-sib.ch/announce/CC corseed and main to literase agreement (See http://www.isb-sib.ch/announce/CC control of literase proposed see agreement (See http://www.isb-sib.ch/announce/CC control of literase proposed see agreement (See http://www.isb-sib.ch/announce/CC control of literase agreement (See ht	CARBOHYD 568 568 N-LINKED (GLCNAC) CARBOHYD 627 627 N-LINKED (GLCNAC) CARBOHYD 789 789 N-LINKED (GLCNAC) CARBOHYD 996 996 N-LINKED (GLCNAC)

CADHERIN 12.

1448

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17 GEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCK----
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      DOMAIN
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                                                                                                                                                                                                                              ·;
•
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               TISSUE=Brain;
MEDLINE-98360089; PubMed=9693030;
MRAyama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O
"Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                      MEDLINE-2020599; PubMed-10716726; Wu Q., Maniatis T.; "Large exons encoding multiple ectodomains are a characteristic feature of protocadharin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                              Poustka A., Wellenreuther R., Mewes H.-W., Weil B., Wiemann S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 32 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; EGF-like domain; Signal
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYDENTIAL.
CADHERIN 1.
CADHERIN 2.
CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
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InterPro: 1PR00126; Cadherin.
InterPro: 1PR00126; EGF-like.
InterPro: 1PR00156; EGF-like.
InterPro: 1PR00159; Laminin_G.
Pfam: PF000028; cadherin; 33.
Pfam: PF000028; CADHERIN.
SWART: SW00112; CA; 32.
SWART: SW00118; EGF: 2.
SWART: SW0018; EGF: 2.
SWART: SW0018; EGF: 2.
PROSITE; PS0023; CADHERIN_1; 14.
PROSITE; PS0023; CADHERIN_2; 32.
PROSITE; PS00186; EGF_1; 2.
PROSITE; PS00186; EGF_2; 1.
TRANSMEMBLY SS0025; LAMIG_DOMAIN; 1.
                                                                                                                                                                   [2]
SEQUENCE OF 3777-4349 FROM N.A.
                                                                                                                                                                                                                                                                                       [3]
SEQUENCE OF 4142-4349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF231022; AAF61928.1; -. EMBL; AB011535; BAA32463.1; -. EMBL; ALIS7443; CAB75663.1; -. Genew; HGNC:3596; FAT2. MIM; 604269; -.
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                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                  2874
                                                                                                                                  2782 SVNIQVGDVNDNRPVFEADPYKAVLTENMPV--GTSVIQVTAIDKDTGRDGQVSYRLSAD 2839
                                                                                                                                                                                                                                                              2875 VVAYDHGQTIQLSSQALVQVSITDENDNAPRFASEEYRGSVVENSEPGELVATLKTLDAD 2934
2724 YSLVRGTTPESNKDG--VFSLDPDTGVIKVRKPMDHESTKLYQIDVMAHCLQNTDVVSLV 2781
                                                                                                                                                                                                                                                                                                                            2935 ISEQNRQVTCYITEGDPLGQFGISQVGDEWRISSRKTLDREHTAKYLLRVTASDGKFQAS 2994
                                                                                                         ---GSL-YHLGAD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 KKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHE
                                                                                                                                                                                                                                                                                               -----QVTSVAFGGPNLDELHVTSAGLQLDDSS---LDKSLVNGHVYRVTGLGVKGFAG
                                                                                                                                                                                                 2840 PGSNVHEL-FAIDSESGWITTLQEL-------DCETCQ-----TYHFH-
                                                                                                                                                                                                                                  VPGYPDGQTI-------DEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                          DKLVSFIIPLAGSPGRFVVSLEREIAIL----TWDGVSAAPTSIEAIVN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 242;
                                                                                                         EPHIKNNRLNDGK----ADPLGNLWTGTMAIDAGLPVGPVT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 91.5; DB 1; 26.8%; Pred. No. 2.8;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002143; Ribosomal_L1.
Pfam; PF00687; Ribosomal_L1; 1.
ProDom; PD001314; Ribosomal_L1; 1.
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Matches 41; Conservative
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30-MAY-2000 (
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P48951;
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Gaps

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Indels

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                                  31 ETSTIKEDGIVEVAFRLGVDPR-----KADQMVRGIVNLPHGICK----TARVLVFATG
ETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLEREIAILTW
                                                                                                                                                          120 LWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMH 152
                                                                               DGVSAAPTSIEAIVNVEPHI ----KNNRLND----
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August 1, 2003, 14:26:38 ; Search time 70 Seconds (without alignments) 906.607 Million cell updates/sec
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1615
1 MGPVVEKIAELGKYTVGEGP.......HVYRVTGLGVKGFAGVKVKL 308
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_nvertebrate:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_archeap:\*

sp\_vertebrate:\* sp\_rvirus:\* sp\_bacteriap:\*

sp\_virus:\*

sp\_organelle:\* sp\_phage:\*

sp\_mammal:\* sp\_mhc:\*

sp\_plant:\* sp\_rodent:\*

	Description	095vi4 photinus pv			_	09vfq5 drosophila	O9vyrl drosophila	Ogndpl sarcophaga	O9bid6 calliphora	09i922 xenopus lae	Ogiba8 xenopus lae	Q9i923 qallus qall	0925w3 rattus norv	Q95pd9 calliphora	Q92zr8 rhizobium m	O8uil2 agrobacteri	. O96zi9 sulfolobus
SUMMARIES	ID	Q95Y14	Q8TA67	Q8TA68	9SQN60	Q9VFG5	Q9VYR1	Q9NDP1	Q9BID6	091922	Q9IBA8	091923	Q925W3	Q95PD9	Q92ZR8	Q8UJL2	612960
	DB	5	2	2	S	5	2	2	Ŋ	13	13	13	11	Ŋ	16	16	17
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ф	Query	100.0	55.1	53.2	35.2	35.2	34.1	33.3	32.3	29.4	29.1	28.3	28.1	27.6	26.2	25.4	24.6
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WIGTMAIDAGL-PVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKR 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of Drosophila homologue of senescence marker protein-30
                                                                                                                  SEQUENCE FROM N.A.
GOMI K., Hirokawa K., Kajiyama N.;
GOMI K., Hirokawa K., Kajiyama N.;
GOMI K., Hirokawa K., Kajiyama N.;
MOJECULIAR CLONING and expression of luciferin-regenerating
(LRE) CDNA in Luciola cruciata and Luciola lateralis.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB07247; BAB85478.1. -
EMBLS 307 AA, 34286 MW; B03CED0AC609A92C CRC64;
                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inser
Pterygota: Neoptera; Endopterygota; Coleoptera; Polyphaga
Elateriformia; Cantharoidea; Lampyridae; Luciola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Last annotation update)
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40.7%; Pred. No. 6.9e-39;
Live 48; Mismatches 116;
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                                                                                                                                                                                                                                                        53.2%; Score 859.5; DB 5
52.8%; Pred. No. 5.5e-63;
iive 58; Mismatches 85
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EMBL, AB029490; BAA92938.1; -
FIYBBSSE, FEGRO038257; SMP-30.
SEQUENCE 303 AA: 33349 MW, 68F12B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Senescence marker protein-30 (SMP-30)
SMP-30 OR CG7390.
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STRAIN-CANTON S; TISSUE-WHOLE BODY;
PubMed-10817837;
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
            Luciola lateralis (Firefly)
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                                                                                                                                                                                                                                                                              Best Local Similarity 52.8
Matches 163; Conservative
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Best Local Similarity
Matches 121; Conservat
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                                                                                    NCBI_TaxID=7052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGPVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLWTGTMAIDAGLPVG-PVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 QQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLG
                  EVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG
VDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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SEQUENCE FROM N.A.

Molecular Loning and expression of luciferin-regenerating enzyme
"Molecular cloning and expression of luciola lateralis.";

(LRE) cDNA in Luciola cruciata and Luciola lateralis.";

SUBMILTER (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB072448; BABB5479.1;

EDDUENCE 309 AA; 33804 MW; BE33C4E2IEF5IE6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
                                                                                                                                                                                                                                                                                                                                                                                     Luciola cruciata (Japanese firefly) (Genji firefly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriformia; Cantharoidea; Lampyridae; Luciola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.1%; Score 889.5; DB 5; Length 309; 56.6%; Pred. No. 1.8e-65; ive 47; Mismatches 83; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created) .01-JUN-2002 (TrEMBLrel. 21, Last sequence update) .01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Luciferin regenerating enzyme.
                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         Luciferin-regenerating enzyme.
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Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKGLPGDRVKL 309
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                           FAGVKVKL 308
                                                                                                                                                              |||||||||||
FAGVKVKL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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RY Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admantides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Admantides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,

RA Admantides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Erandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Gorson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Barris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A.,

RA Liu X., Mattei B., McIntosh T.C., McLood M. P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLood M. P., Mopherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remighor K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                    SNQRPLFTFEK -- HEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPD 251
            73
                                                                                                                                                                                                                                                  PQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVKL 308
                                                                                                                                                                                                                                                                  253 TQITSVAFGGPNLDILYVTTA-----NKFDQPKPAGTTFQVTGLNAKGYAGVNLKI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                          134 GPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSI
         VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDK--LVSFIIPLAGSPGRFVV
                                                                     SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spralling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Wenter R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           CG7390 protein (RE17477p).
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74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 SNPKVIFDLRKIRPEGPLFPDGMTVDTDGNIYVATFNGGTVFKVNPSTGKILLE-IKIPT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDK--LVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 GPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSI
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (Regucalcin HOMOLOGUE).
REGUCALCIN OR CG1803.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta:
Pteryota: Meoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 LGEGPHWDVDRQSLYYVDLESAGINRYDFKQNKVYRAKIEGEIFASFILPVENKPQEFAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBqn0038257; smp-30.
SEQUENCE 303 AA; 33377 MW; 68F92692E1AC88AD CRC64;
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40.7%; Pred. No. 6.9e-39;
ive 48; Mismatches 116;
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Matches 121; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
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Celniker S.;
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296
                                                                                                                                                                                                                   SEQUENCE
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Q9BID6
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Dunb P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kaipen G.H., Ke Z., Kuhp D., Hair K.,
Alali M., Kalush F., Karpen G.H., We Z., Kuhp D., Lai Z.,
Alali M., Kalush F., Karpen G.H., We Z., Kuhp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Marttei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Marttei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Marttei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rhe B.C., Siden Krämos I., Simpson M., Strong R., Sun B.,
Spier E., Spradling A.C., Staphetton M., Strong R., Sun E.,
Rhulljams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao, Q., A.,
Rheng Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rheng Z.-Y., Wassarman D.A., Weinstock G.W., Weissenbach J.,
Rheng Z.-Y., Wassarman D.A., Weinstock G.W., Weissenbach J.,
Rheng Z.-Y., Wassarman D.A., Weinstock G.W., Weissenbach J.,
Rheng X.H., Zhong K.N., Zhong W., Zhong X., Zhon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPV----TGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDAS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 KIPDDQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFAGVKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LGEGPHWDVARQSLYYVDLEAGSLLRYDYAQNKVYKTKIEGETLAGFVLPVEGRPQEFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Identification and characterization of an anterior fat body protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F9AD6EB15E758209 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 550; DB 5;
Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20250851; Pubmed=10788801; Nakajima Y., Natori S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003487; AAF48129.1; -.
EMBL; AB036904; BAA99283.1; -.
FlyBase; FBGn0030562; requesalcin.
SEQUENCE 303 AA; 33644 MW; F95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127:901-908(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.1%;
39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 L 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in an insect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
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Best Local S
Matches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
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Q9NDP1
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AA.

PRT;

PRELIMINARY;

Q9NDP1 Q9NDP1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AIPVEGTTDQFAVGSGRRVVIVQWDGISETAKVIKTLFEVQTGDERFNGNRFNDGKCDPR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-ANTERIOR FAT BODY;
Hansen I.A., Mayer S.R., Schaefer I., Scheller K.;
Hansen I.A., Mayer S.R., Schaefer I., Scheller K.;
Identification of the anterior fat body protein as interactor of the hexamerin receptor in the blowfly Calliphora vicina.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY028616; AAR26774.1;
SEQUENCE 306 AA; 34289 WW; 497241A2424C2C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STQQPEVLLDTVKIPDPQVTSVAFGGPNIDELHVTSAGLQLDDSSLDKSLVNGHVYRVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina). Bukaryota; Metazoa; Arthropoda Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroldea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV:--DKLVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY - - PDGQTIDEEGNLWVAVFQGQRIIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Anterior fat body protein.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora
                                                                                                                                                                                                                                                                                                                                   Nakajima Y., Natori S.; "Identification and characterization of an anterior fat body protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; Score 538; DB 5; Length 30
39.0%; Pred. No. 2.1e-36;
.ive 48; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  J. Blochem. 127:901-908(2000).
EMBL, AB036903; BAA99282.1; -.
SEQUENCE 306 AA; 34319 MW; 77CFF54575D7E8E7 CRC64;
                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
  Created)
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                                                                                                                                                                                                                                                                                    TISSUE=FAT BODY;
MEDLINE=20250851; Pubmed=10788801;
(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || ||: |::|
294 LGAKGYPMTKIQL 306
                                                                     Anterior fat body protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGVKGFAGVKVKL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.3'
Best Local Similarity 39.0'
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                              N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   in an insect."
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74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 RPAVVERNQGSLFTLYPDHSVVKHFDMVDISNGLDWSLDHKTLYYIDSLSFKVDALDYDM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20133502; PubMed=10727865; Sato A., Asashima M., Yokota T., Nishinakamura R.; Sato A., Asashima M., Yokota T., Nishinakamura R.; Sato A., Asashima and expression pattern of a Xenopus pronephros-specific gene, XSMP-30."; Pub. 92:273-275(2000).

EMBL; AB033368; BAA93719.1; BABB9749258BB41C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
    247 VKIPDDQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA 302
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.1%; Score 470.5; DB 13; Length 36.8%; Pred. No. 7.9e-31; Live 47; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 AA
                                                                                                              299
                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20351777; PubMed=10891565;
                                                                                                                                                                                         Senescence marker protein-30.
XSMP-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misawa H., Yamaquchi M.;
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regucalcin.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 109; Conserva
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-ANIMAL CAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                              Q9IBA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus
                                                                              RESULT 10
Q9IBA8
ID Q9IBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
                                                                                                                                                                                                           178 KRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY--PDGQTIDEEGNLWVAVFQGQRIIKI 235
                                                                                                                                                                                                                                                                                                                                     241 NPTTGQVLLE-IKFPCKQITSAAFGGPNFHILFVTTS-----SRFGEPHPAGTTYKVTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AMGNIFSALNWE-----DQSVITILARVDEDKPNNRFNDGKVDPEGRFLAGTMSQE----I 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLNDGKADPL 117
                                                                                                                                                        62 AVPVEGTTDQFAVGSGRRVVIVQWDGVSETAKVLKTLFEVQTGDERFTGNRFNDGKCDPR 121
                                                                                                                                                                                        GNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSG 177
                                                                                                                                                                                                                                                                                                                   STQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTG 295
                                                                             3 PVVEKIAELGKYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKV--DKLVSF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 YTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YKIGESPVWEEKEGTLLFVDITGQKVCRWDPSTKKVQSVSVEAPIGSV--ALRKSGGYVL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misawa H., Yamaguchi M.; "The gene of Ca2+-binding protein regucalcin is highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 299;
 Score 521; DB 5; Length 306;
Pred. No. 5.4e-35;
1; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vertebrate species.";
Int. J. Mol. Med. 6:191-196(2000).
EMBL; AB037936; BAA90694.1;
SEQUENCE 299 AA; 33087 MW; BABB9749258BB2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        091922;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.4%; Score 474.5; DB 13; Best Local Similarity 37.2%; Pred. No. 3.7e-31; Matches 110; Conservative 46; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20351777; PubMed=10891565;
                               44;
32.3%;
                                                                                                                                                                                                                                                                                                                                                                                  LGVKGFAGVKVKL 308
                                                                                                                                                                                                                                                                                                                                                                                                    || ||: |::|
LGAKGYPMTKIQL 306
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                               122;
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196 HSIYKINPTTGQVLLE-IKFPCKQITSAAFGGNFHILFVTTS-----SRFGEPHPAGT 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 YYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGY···PDGQTIDEEGNLWVAVFQG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 QRIIKISTQQPEVLLDTVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGH 289
PTGQISNRRTVYKMEKDE--QIPDGMCIDVEGKLWVACYNGGRVIRL---DPETGKRLQT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLAGFAVPVEGTTDQFAVGSGRRVVIVQWDGVSETAKVLKTLFEVQTGDERFTGNRFND 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 DKLVSFIIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNV---EPHIKNNRLND
                                                                                                                                                                                                                                                                                AFP.

Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).

Bukaryota; Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta;

Pterygota; Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha:

Oestroidea: Calliphoridae: Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Hansen I.A., Meyer S.R., Berlinger M.J., Scheller K.;
Hansen I.A., Meyer S.R., Berlinger M.J., Scheller K.;
Indentification of new interactors of the hexamerin receptor in the blowfly Calliphora vicina.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF326959; AAK51353.1; •.
                                      VKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKGFA
                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Putative calcium binding transcriptional regulatory protein.
RA0381 OR SMA0717.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid PSyMA (megaplasmid 1).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae: Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 267;
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Last annotation update)
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39.4%; Pred. No. 7.8e-29;
live 37; Mismatches 107;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
Anterior fat body protein (Fragment)
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249 TYKVTGLGAKGYPMTKIQL 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AA; 29836 MW;
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102; Conservative
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Q95PD9
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                                                                                                                                                                                                                                                                                          VGPVT-----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYD 187
                                                                                                                                                                                                                                                                                                                                                                ASTLSISNQRPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVKIPDPQVTSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGHVYRVTGLGVKG---- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                           72
                                                                                                                                                                                                                              RYRLGESPVWDEKENSLLCVDITGRKVCRWDAASGQVQALSVDAPVSSV--ALRKSGDYV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 YIVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 YRCGESPVWEEASKCLLEVDIPSKTVCRWDSISNRVQRVGVDAPVSSV--ALROSGGYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 SLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 IIGTKFCALNWE-----DQSVFILAMYDEDKKNNRFNDGKVDPAGRYFAGTMAEE----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 GPVT----GSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 STLSISNORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEV--LLDT
                                                                                                                                                                                             13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFV
                                                                                                                                                                                                                                                                   73 VSLEREIAILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLP
                                                                                                                                                         Gaps
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"The gene family encoding the calcium-binding protein regucalcin.";
"The gene family encoding the EMBL/GenBank/DDBJ databases.
EMBL; AB037934: BAA90692.1; -- SEQUENCE 299 AA; 33390 WW; 5D8F2D95FCA4EE35 CRC64;
         conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.1%; Score 453.5; DB 11; Length 299; 37.5%; Pred. No. 2e-29;
                                                                                                                    Length 299;
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                                                                                                                                                        Indels
     "The gene of Ca2+-binding protein regucalcin is highly
                                        Int. J. Mol. Med. 6:191-196(2000).
EMBL, AB037935; BAA90693.1; -.
SEQUENCE 299 AA; 33229 MW; 4754C7571164720E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                  28.2%; Score 455; DB 13; 37.0%; Pred. No. 1.5e-29; ive 40; Mismatches 123;
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       "The gene or vertebrate species.";
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Mammalla; Eutheria; Rodentia;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 NEGLIVASQDGVEHFDFDRGDFNPFAEP-----EPGLPENRLNDAKVDPSGRLWYG
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                                           Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.,
Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSyma megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL: AE007229; AAK65039.1; -
Interpro: IPRO02885; HTH_ICIR.
Pfam: PF001614; ICIR: 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 569 AA; 60943 MW; EB34C90D654EEBAD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 569;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transcriptional regulator, IclR family/regucalcin.
ATU5464 OR AGR_PAT_685.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                     26.2%; Score 423.5; DB 16; 34.6%; Pred. No. 1.6e-26; live 46; Mismatches 102;
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                       MEDLINE-21396509; PubMed-11481432;
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Matches 100; Conservative
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NCBI_TaxID=176299;
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SEQUENCE FROM N.A.
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EMBL: ABO08967; AAL46151.1; ALT_INIT.
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33.1%; Pred. No. 2.4e-25;
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US-09-548-372D-51
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88.5
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DB
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Sequence 5111, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LWTGTMAIDAGLPVGPVTGSLYHLGAD-KKVKMHESNIAIANGLAWSNDLKKMYYIDSGK 178
                                                                                                    58, Appl
58, Appl
4705, Appl
4705, Appl
1, Appli
9, Appli
53, Appli
53, Appli
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Appl
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Appli
Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 NRLHRIALEDDGVTIAPFGATIPYYFTGHE---GPDSCCIDSNDNLYVAMYGQGRVL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                              Sedinence Sedine
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                           US-08-747-221B-14

US-09-005-051-14

US-08-747-221B-58

US-08-747-221B-58

US-09-105-051-58

US-09-134-001C-4705

US-09-134-001C-4705

US-09-135-06-1

US-09-1489-506-1

US-09-1489-506-1

US-09-1489-506-1

US-09-147-221B-53

US-09-005-051-19

US-09-005-051-19

US-09-333-6278-1

US-09-333-6278-1
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Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEERAL INCORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST;
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4646, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%;
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71 VEPY----QLEGRQAQILKHHYNSLVAENAMKPVSLQPREGEWNWEGADKIVEFARKHNM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : ||: | : ||: || | : || ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 VEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVG--PVTGSLYHLGADKKVKM-HESNI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 AIA-NGLAWSNDLKKMYYID-SGKRRVDEYDYDASTLSISNQRPLFTFEKH---EVPGYP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ELRFHTLVWHSQVPEWFFIDENGNRMVDETDPEKR--KANKOLLLERMENHIKTVVERYK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 P---EVLLDTVK-----IPDPQV---TSVAFGGPNLDELHV-----TSAGLQLDDSSLD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D------GQTIDEEGNL----WVAVFQGQRIIKI---------STQQ
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APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.8%; Score 93; DB 4; Best Local Similarity 24.7%; Pred. No. 0.089; Matches 60; Conservative 36; Mismatches 8
                                                                                  CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-0057.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
               UMBER: US/08/501,126
29-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-282-197C-55; Sequence 55, Application US/08282197C; Patent No. 5871730; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryszard
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1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS;
                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cimbala, Michele A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brzezinski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-501-126-2
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CORRESPONDENCE ADDRESS:
                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------TWDGVSAAPTSI-EAIVNVEPHIKNNRLNDGKADPLGNLWTG--TMAIDAGL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VSNSHGGNQLDGKSNQYKSVHDMIKDVSPAIV-GVINMQKSTNLDDLFNGKASKSKEAGI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSIS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 GIKAIQFANSSKVQTGDSVFAMGNPLGLEFANS------VTSGIISASERTIDANTSAGN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NORPLFTFEKHEVPGYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VGINSMKIAAAQV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 EKNOHHYRNSSOKRHTFPWIKTIIVAII--AGIIGALLVLGIGKLLNKTGFNNEGATVHQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SLEREIAIL--
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF EX DID NOS: 5674
LENGTH: 413
LENGTH: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 94; DB 4; Length 413;
; Pred. No. 0.074;
46; Mismatches 101; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 PVGPV----TGSLY-----HL--GADK-KVKMHESN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 413;
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EGIGFAIPS-NEVRVILEQLVKHGKIERPSIGIGLIN 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 TSVAFGGPNLDELHVTSAGL----QLDDSSLDKSLVN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 EKTFHKY-VPSQKKYTFCKVDKLVSFIIPLAGSPGRFVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herweijer, Margaretha A.
Van Beckhoven W.C., Rudolf F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Morrison & Foerster
2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herbes, Wilhelmina T.
Van Der Kleij, Wilhelmus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 TKVNVLQTDAAINPGNSGGALVDINGNL--
                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Staphylococcus epidermidis US-09-134-001C-5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Solingen, Pieter
Williams, Diane P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08501126
Patent No. 6140095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iverson, Sara
Farrell, Roberta L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ones, Brian E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.6%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20006-1812
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APPLICANT: Van SC
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US-08-501-126-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Gaps

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GENERAL INFORMATION:

APPLICANT: UDAKA, Shigezo

APPLICANT: SAKAGUCHI, Kenji

APPLICANT: PANAGATA, Hideo

APPLICANT: PEKKER, Koen

TITLE OF INVENTION: XYLOSEISOMERASE GENE OF THERMUS

TITLE OF INVENTION: RUGATIONS XYLOSEISOMERASE AND PROCESS FOR PREPARATION OF

TITLE OF INVENTION: FRUCTOSE

CORRESPONDENCE ADDRESS:

ADDRESSEE: BUINS, Doane, Swecker and Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
      -----VNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKK 148
                                                                                                    722 RHNLYSAQQMTVGPKSKN------PLEGLTAGAYEIEAEVEI-PANSSVTEFGFQLR 771
                                                                                                                                                     149 VKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVP 208
                                                                                                                                                                                  209 GYPDGQTIDEEGNLWVAVFQGQRIIKISTQQPEVLLDTVKIPDPQVTSVAF---GGPNLD 265
                                                                                                                                                                                                                                                                                    813 LKPENQKVK-----LRIFVDESSVEVFGNDGKVVFSDVIFPDPAGRAMAFYSLGG---- 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%; Score 89.5; DB 1;
19.8%; Pred. No. 0.21;
ive 57; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024705-007
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/783,150
FILING DATE: 28-CCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FULLING DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08112630 Patent No. 5411886
                                                                                                                                                                                                                                                                                                                                 ELHVTSAGLQLDDSSLDKS 284
                                                                                                                                                                                                                                                                                                                                                                         863 EVKVSSMKVYALDNIWRKS 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexander STATE: Virginia COUNTRY: United States ZIP: 22313-1404
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amino acid
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Best Local Similarity 19.8
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-112-630-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rea, Teresa S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-112-630-2
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                                                                                                                                                                                                                                                                                                                                                                                    71 VEPY----QLEGRQAQILKHHYNSLVAENAMKPESLQPREGEWNWEGADKIVEFARKHNM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDVTSWDVVNEVIDDGGGLRESEWYQI-TGTDYIKVAFETARKYGGEEAKLYINDYNTEV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303
                                                                                                                                                                                                                                                                                                                                              100 VEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLP--VGPVTGSLYHLGADKKVKM-HESNI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                   157 AIA-NGLAWSNDLKKMYYID-SGKRRVDEYDYDASTLSISNQRPLFTFEKH---EVPGYP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...-STQQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P---EVLLDTVK-----IPDDPQV---TSVAFGGPNLDELHV----TSAGLQLDDSSLD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 PSKRDDLYNLVKDLLEQGVPIDGVGHQSHIQIGWPSIEDTRASFEKFTSLGLDNQVTELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 VPSQKKYTFCKVDKL-VSFIIPLAGSPGRFVVSLEREIAILTWD-GVSAAPTSIEAI---
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                        64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INPORTATION:
APPLICANT: Moller, Soren
APPLICANT: Moller, Soren
APPLICANT: Johansen, Charlotte
APPLICANT: Hoek, Lisbeth Hedegaard
TITLE OF INVENTION: A 2,6,-D-D-Fructan Hydrolase Enzyme
TITLE OF INVENTION: Process For Using The Enzyme
TITLE OF INVENTION: Process For Using The Enzyme
TILLE OF INVENTION: Process For Using The Enzyme
CURRENT APPLICATION NUMBER: US/09/397,885
CURRENT FILING DATE: 1999-09-17
EARLIER APPLICATION NUMBER: PA 1998 01173
EARLIER FILING DATE: 1998-09-18
EARLIER FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: 60/101,615
EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 90; DB 4; Length 1277; 21.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                           5.6%; Score 91; DB 2; Length 397; 24.7%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                        84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-----GQTIDEEGNL----WVAVFQGQRIIKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 102;
                                                                                                                                                                                                                                                                                                        Mismatches
33,851
3R: 1050.0410000
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REGISTRATION NUMBER: 33,851
REPERENCE/POCKET UNBER: 1050
TELECOMMULCATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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US-09-397-885-3
                                                                                                                                                   : 397 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                      60; Conservative
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 KSL 285
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                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                              Query Match
Best Local 9
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APPLICANT: GURNEY ET AL.

APPLICANT: GURNEY ET AL.

TITLE OF INVENTATION:
TITLE OF INVENTATION: THEREOF
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR PELICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 FGGPN--LDELHVTSAGL-----QLDDSSLDKSLVNGHVYRV----TGLGVKGFAG 303
                                                                                                                                               TITLE OF INVENTION: FIERRONECTIN AND FIBRINOGEN BINDING PROFEIN FROM GROUP, ITILE OF INVENTION: STREPTOCOCCI
FILE REPERENCE: 022927-006
CURRENT APPLICATION NUMBER: US/09/327,536
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: US 08/714,402
PRIOR APPLICATION NUMBER: US 08/714,402
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | : | | : | | | : | 860 TTVEDSRPVDTLSGLSSEQGQSGDMTIEEDSAT-------HIKFSKRDIDGK 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 KYTVGEGPHWDHETQTLYFVDTVEKTFHKYVPSQKKYTFCKVDKLVSFIIPLAGSPGRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLEREIAI - - - - - LTWDGVSAAPTSIEAIVNVEPHIKNNR- - - - LNDGKADPLGNLWTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
5.4%; Score 88; DB 4; Length 1161;
Best Local Similarity 17.5%; Pred. No. 1.9;
Matches 64; Conservative 55; Mismatches 122; Indels 124;
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Patent No. 6420534
Sequence 2, Application US/09327536 Patent No. 6355477
                                    Patent No. 6355477
GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
APPLICANT: ROCHA, Claudia
                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: SFFBP gene
US-09-327-536-2
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US-09-548-372D-51
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SEQ ID NO 2
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Sequence 3945, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION:
FILLE OF INVENTION:
FILL OF INVENTION:
FILLE OF INVENTION:
FILL OF INVENTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | :: | :: | :: | SALKAAFFLYDLLESSGYQGPRHFDAHALRTEDEEG-VWAFARGCMRTYLLLKERAEAFR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 NDGK---ADPLGNLWTGTMAIDAGLPVGPVTGSLYHLGADKKVKMHESNIAIANGLAW-- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SNDLKKMYYIDSGKRRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPDGQTID 217
                                                                                                                                               80 AILTWDGVSAAPTSIEAIVNVEPHIKNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTGS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 ISNORPLFTFEKHEVPGYPDG-----QTIDEEGNLWVAVFQGQRIIKISTQQPEVLL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E----DPEVKELLAAYYQEDPAALALLGPYSRE---KAEALKRAELPLEAKRRGYALE 372
                                                                                                                                                                                                                                                                                              154 ----WDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFAT------VGSMLAF 201
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         38 VVHKLAELGAYGVNLHDEDLIPRGTPPQERDQIVRRFKKALDETGLKVPMVTANLFSDPA
                                                                                                       -----FIIPLAGSPGRFVVSLE-----REI
                                                                                                                                                                                                                                                                                                                                                                                                        DTVKIPDPQV-----TSVAFGGPNLDELHVTSAGLQLDDSSLDKSLVNGH-VY
                                                                                                                                                                                                                                                                                                                                                             140 LYHLGADKKVKM----HE--SNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLS
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22.8%; Pred. No. 2.6;
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3945
                                                                                                          46 QKKYTFCKVDKLVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVTGLGVKGFAGVK 305
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Matches 54; Conservative
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US-09-327-536-2
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GENERAL INFORMATION:

APPLICANT: GURREY ET AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

TITLE OF INVENTION: THEREFE

TITLE OF INVENTION: THEREFE

CURRENT APPLICATION NUMBER: US/09/548,372D

CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/155,493

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 60/101,594

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 73

SEQ ID NOS: 73

SEQ ID NOS: 73

SEQ ID NOS: 73

SEQ ID NOS: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
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   112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAA1TESDKF 169
                                                                           97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
                                                                                                                                                      -----GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 211
                                                                                                                                                                                                                                                                                                    212 IGGIDH------SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
PatentIn version 3.1
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APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/480372D
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 IGGIDH------SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                            112 YYQRQLSSTYRDLRKGV--YVPYTQCKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                                                                                                                                                                                                            58 GSFVEMVDNLRGKSGQGYYVEMTVGSPP-----QTLNILVDTGSSNFAVGAAPHPFLHR 111
                                                                                                                                                                                                                                                                                                                                                                                                       97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI-------DAGLP-----VGPVTGSLY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 21.1
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                                                                                                                                                                                                                                                                                                 42 YVPSQKKYTFCKVDKLVSFIIPLA-----GSPGRFVVSLEREIAILTWDGVSAAPTSIEA
                                                                                                                                              Gaps
                                                                                                                                              97;
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                                                                                             Length 476;
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                                                                                             DB 4;
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                                                                                        Score 86.5; DB
Pred. No. 0.64;
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PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR APPLICATION NUMBER: POT/US99/2081
PRIOR APPLICATION NUMBER: POT/US99/2081
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-44
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATCHIN VETSION 3.1
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 73, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
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                                                                                                Query Match 5.4%;
Best Local Similarity 22.0%;
Matches 63; Conservative 3
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TYPE: PRT
ORGANISM: Homo sapiens
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Matches 63; Conserv
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                                                US-09-548-372D-6
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APPLICANT: GIRNEY ET AL.

GENERAL INFORMATION:

APPLICANT: GIRNEY ET AL.

TITLE OF INVENTION: ALZHEINER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES;

TITLE OF INVENTION: ADMER: US/09/548,372D

CURRENT PELING DATE: 29915/62801

CURRENT PELING DATE: 2000-04-12

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARRE: PATENTIN VERSION 3.1

SEQ ID NO 6
                                  TITLE OF INVENTION: THEREOF
TITLE OF INVENTION UNMBER: US/09/548,367D
CURRENT APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 IGGIDH-----SLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GSFVEMVDNLRGKSGQGYYVEMTVGSPP-----QTLNILVDTGSSNFAVGAAPHPFLHR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
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Matches 63; Conservative
                             GURNEY ET AL
     GENERAL INFORMATION:
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US-09-548-372D-6
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Sequence 6, Application US/09548367D

Sequence 6, Application US/09548367D

Sequence 6, Application US/09548367D

GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

CURRENT FILING DATE: 29915/6280H

PRIOR FILING DATE: 1999-09-23

PRIOR PLING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LEMETH: 476
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112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
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                                                          191 L--SISNQR-PLFTFE-----KHEVPGYPDGQTIDEEGNLWVA 225
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US-09-548-367D-6
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Sequence 4, Appli Sequence 13724, A Sequence 6, Appli

Sequence Sequence

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US-09-795-847-53
US-09-794-743-53
US-09-794-925-53
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US-09-794-748-6
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US-09-934-888-60
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US-09-873-4
US-10-027-806-4
US-10-037-801-4
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US-10-037-801-4
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US-09-870-962-2
US-10-165-696-2
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAMA, JUN
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, WASAHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NOWBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Matches 84;
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ORGANISM:
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                                                                                                  August 1, 2003, 14:35:09 ; Search time 47 Seconds (without alignments) 778.256 Million cell updates/sec
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US-09-794-927-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/10160758
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VTGSLYHLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISN 195
                                                                          GGGTLSRLAPDGTARTVLDDVTISNGVGWSPDGRLMYFNDTPTRRIDVFDVDEDGRPV-G 182
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US-09-969-362-3
: Sequence 3, Application US/09969362
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238 TACAFGGAGLTDLYITTA 255
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                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 1320cm, 1230cm, 1200cm, 121TLE OF INVENTION: 120cm, 
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21.2%; Pred. No. 7.4;
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PRIOR APPLICATION NUMBER: 60/111,675
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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APPLICANT: SAKRI, YOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                       Johansen, Charlotte
Schafer, Thomas
Ostergaard, Peter Rabbek
Hoeck, Lisbeth Hedegaard
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HORIKAWA, HIROSHI
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APPLICANT: OMURA, SATOSHI
US20020076790A1
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154 SNIAIANGLAWSNDLKKMYYIDSGKRRVDEYDYDASTLSISNQR--PLFTFEKH--EVPG 209
                                   111 DGKADPLGNLWTGTMAID---AGL-------PVGPVTGSLYHLGADKKVKMHE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 DGQSDGKSSIWTDTFAIDDTASGLRLVSYRLRLTLYRTPGGGITPTVWRLGA----- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 RRVDEYDYDASTLSISNQRPLFTFEKHEVPGYPD-----GQTIDEEGNLWVAVFQGQRII 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 YPDGQTIDEEGNLWVAVFQGQRIIKISTQQP---EVLLDTVKIPDPQVTSVA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 YDNG-----GEAWCSPTSSQMIIEYWGRRPTPGQLAWVDPSYADPQVCHAA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.4%; Score 87; DB 15; Length 450; Best Local Similarity 22.1%; Pred. No. 3; Matches 38; Conservative 23; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: ISHERAWA, JUN
APPLICANT: ISHERAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATORI, YOSHIYUKI
APPLICANT: APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                      Sequence 14443, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6671, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                       EVTNESPROPIG-VGLPDPEHT 558
                                                                                             234 KISTQQPEVLLDTVKIPDPQVT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14443
                                                                                                                                                                                                                              US-10-156-761-14443
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                                                                                                                                                                                                                                                 44 PSQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLEREIAILTWDGVSAAPTSIEAIVNVEPH 103
                                                                                                                                                                                                                                                                               68 PGR-----FVVSLEREIA---ILTWDGVSAAPTSIEAIVNVEPHIK------ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 VAGPENNDTDFTWDEFVRRVNNELANGWGNLVNRTVSM-AHKNFGEVPVPGALEE--SDK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 YIVGEGPHW-----DHETQTLYFVDTVEKTFHKYV-PSQKKYTFCKVDKLVSFIIPLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 115;
                                                                                                                                                                                                       15;
                                                                                                                                                               Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 88.5; DB 11; Length 610;
21.7%; Pred. No. 3.4;
Live 48; Mismatches 89; Indels 115
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                        104 IKNNRLNDGKADPLGNLWTGTMAID---AGLPVGPVTG 138
                                                                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                        5.5%; Score 89.5; Di
26.5%; Pred. No. 1.5;
                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-11-6
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PARCHING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4495, Application US/09738626
Publication No. US20020197605A1
                                                                                           ; ORGANISM: Streptomyces avermitilis US-10-156-761-12646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIKO
APPLICANT: IKEDA, MASATO
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Best Local Similarity 21.78
Matches 70; Conservative
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12646
LENGTH: 418
                                                                                                                                                                               Similarity 26.5%
26; Conservative
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                                                                                                                                                        Query Match
Best Local S
Matches 26
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APPLICANT: Parodi, Luis A.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 2841/62800 PARODICATION NUMBER: US/9/795,847
CURRENT APPLICATION NUMBER: US/416,901
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR APPLICATION NUMBER: 06/155,493
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR PRIOR APPLICATION NUMBER: 06/101,594
PRIOR PRILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-----EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 FIN-----GSNWEGILGLAYAEIARLCGAGFPLNOSEVLASVGGSMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 IGGIDH------SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
                                                                                                                                               142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD------EYDYDAST 190
                                                                                                                                                                        212 IGGIDH------SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GPVVEKIAEL-----GKY---TVGEGPHWDHETQTL-YFVDTVEKTF------HK 41
112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                --DAGLP-----VGPVTGSLY 141
                                                                                              --GSNWEGILGLAYAEIARLCGAGFPLNOSEVLASVGGSMI 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b); OTHER INFORMATION: delta TM US-09-795-847-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
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                                                                                                                                                                                                                                                191 L--SISNQR-PLFTFE-----KHEVPGYPDGQTIDEEGNLWVA 225
                                                                                                                                                                                                                                                                                 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 86.5; DB 10; 22.0%; Pred. No. 3.2;
                                                     97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application US/09795847 Patent No. US20010018208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J
APPLICANT: Heinrikson, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.4%
Best Local Similarity 22.0%
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver.
SEQ ID NO 51
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                                                                                                   170 FIN----
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TITLE OF INVENTION: ALLHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 2841/62808
FILE REFERENCE: 2841/62808
CURRENT APPLICATION NUMBER: 05/416,901
PRIOR APPLICATION NUMBER: 60/15,493
PRIOR PILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                            81 ILTWDGVSAAPTSIEAIVNVEPHI--KNNRLNDGKADPLGNLWTGTMAIDAGLPVGPVTG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GPVVEKIAEL-----GKY---TVGEGPHWDHETQTL-YFVDTVEKTF------HK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 YVPSQKKYTFCKVDKLVSFIIPLA----GSPGRFVVSLEREIAILTWDGVSAAPTSIEA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
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                                                                                                                                                                                                                                                                                                                             DB 11; Length 467;
                                                                                                                                                                                                                                                                                                                                                                           26; Indels
                                                                                                                                                                                                                                                                                                                        Score 87; DB 1
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
     PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6671
                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 SLYHLGADKKVKMHESNIAIA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : ||:: | :| | 437 RVGYQPADRRKPMRFNNTAAA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bienkowski, Michael J.
Heinrikson, Robert L.
Parodi, Luis A.
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.8%;
Matches 29; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 63; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                               US-09-738-626-667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-794-927-51
                                                                                                                                                                                                          LENGTH: 467
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APPLICANT: PATOLI, LUIS A.
APPLICANT: Van, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/62801
CURRENT APPLICATION NUMBER: US/99/794,748
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
SPRIOR FILING DATE: 1998-09-24
NUMBER: OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VEY: 2.0
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APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Beinkowski, Michael J.
APPLICANT: Parofi, Luis A.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: 00941/62901
CURRENT APPLICATION NUMBER: US/09/16,901
PRIOR APPLICATION NUMBER: 60/155,493
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Best Local S
Matches 63
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TITLE OF INVENTION: THEREFOR
FILE SEFERENCE: 2834J/620BC
CURRENT APPLICATION NUMBER: US/09/794,743
CURRENT APPLICATION NUMBER: US/09/794,743
FRIOR PELICATION NUMBER: 09/416,901
PRIOR PELING DATE: 1999-10-13
PRIOR PELING DATE: 1999-10-13
PRIOR PELING DATE: 1999-09-23
PRIOR PELING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR SECULOR NUMBER: 60/101,594
PRIOR SECULOR NUMBER: 60/101,594
PRIOR SECULOR NUMBER: 09/404,130
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER OF SECULORS: 73
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263 VDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQA 308
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Patent No. US2002037315A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
                                                                                                                                                                             Sequence 51, Application US/09794743 Patent No. US20010021391A1
                                                                                                                                                                                                                                                                                             APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
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Best Local Similarity 22.0%
Matches 63; Conservative
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TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US TITLE OF INVENTION: THEREFOR FILE REFERENCE: 28341/6280M CURRENT APPLICATION NUMBER: US/09/869,414
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR PILLING DATE: 1999-10-13
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                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b); OTHER INFORMATION: delta TM
US-09-681-442-51
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OTHER INFORMATION: delta TM
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                                                                                                                                                                                 Length 428;
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                                                                                                                                                                           ch 5.4%; Score 86.5; DB 10; 1 Similarity 22.0%; Pred. No. 3.2; 63; Conservative 31; Mismatches 95;
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PRIOR PILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/09869414
Publication No. US20030077226A1
GENERAL INFORMATION:
APPLICANT: Beinkowski et al.
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         ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2
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US-09-869-414-51
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                                                                                                                                                                                 Query Match
Best Local 8
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APPLICANT BLENKOWSKI, Michael J.
APPLICANT HEINTHEOF ILLIS A.
APPLICANT PAROIL LUIS A.
APPLICANT PAROIL LUIS A.
APPLICANT PAROIL SALISEBER SECRETASE, APP SUBSTRATES THEREFOR, AND USES TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR STATES THEREFOR, AND USES TITLE OF INVENTION: THEREFOR STATES SECRETASE, APP SUBSTRATES THEREFOR, AND USES TITLE OF INVENTION: UNBER: US/09/681,442
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GSFVEMVDNLRGKSGQGYYVEMTVGSPP-----QTLNILVDTGSSNFAVGAAPHPFLHR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 YYQRQLSSTYRDLRKGV--YVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 IVNVEPHIKNNRLNDGKADPLGNLWTGTMAI------DAGLP-----VGPVTGSLY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 FIN------GSNWEGILGLAYAEIARLCGAGFPLNQSEVLASVGGSMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 HLGADKKVKMHESNIAIANGLAWSNDLKKMYYIDSGKRRVD-------EYDYDAST 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 IGGIDH-----SLYTGSLWYTPIRREWYYEVIIVRVEINGODLKMDCKEYNYDKSI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 YVPSQKKYTFCKVDKLVSFIIPLA----GSPGRFVVSLEREIAILTWDGVSAAPTSIEA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Hu-Asp2(b); OTHER INFORMATION: delta TM
US-09-794-925-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.4%; Score 86.5; DB 10; Length 428; Best Local Similarity 22.0%; Pred. No. 3.2; Matches 63; Conservative 31; Mismatches 95; Indels 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 VDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GPVVEKIAEL-----GKY---TVGEGPHWDHETQTL-YFVDTVEKTF-
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                        SOFTWARE: 1
SEQ ID NO 51
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                       US-09-041-886-16
US-09-381-11-304
US-08-633-993A-12
US-08-844-188-12
US-09-378-088A-12
US-08-232-538-5
US-09-427-353-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      US-08-149-097D-24
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US-08-450-562-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Foley & Lardner: 1800 Diagonal Road, Alexandria
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7218 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-232-463-14/C
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STREET: 18
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STATE: VI
COUNTRY:
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Query Match
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7, Appl
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   (without alignments)
   4497.926 Million cell updates/sec
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Sequence 85,
Sequence 42,
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Sequence 6
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
                version 5.1.6 - 2003 Compugen Ltd.
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US-09-378-088A-85
US-08-844-188-42
US-09-378-088A-39
US-09-345-882-1
US-09-345-882-1
US-09-434-408-3
US-09-453-702B-206
US-09-453-702B-261
US-08-461-52-4
US-08-844-188-37
US-08-961-52-4
US-08-961-53-7
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US-08-961-527-151
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US-08-257-073-14
US-08-235-836C-35
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US-09-660-299-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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1496 ACACTGTAGCACCAGTTGTACCCGATTTAAGTAGTGACATTGATACTAGTAATTTTGATG 1555
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3.9%; Score 35.8; DB 4; Length 1114;
Best Local Similarity 45.5%; Pred. No. 0.34;
Matches 127; Conservative 0; Mismatches 152; Indels 0.
                                                                                                                                                               Length 4739;
                                                                                                                                                             Score 42.2; DB 3; Length 4
Pred. No. 0.0076;
0; Mismatches 148; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/378,088A CURRENT FILING DATE: 1999-08-20
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VENTION: Pesticidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-08-20
IMBER: US 08/633,993
1996-04-19
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US-09-378-088A-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08, PRIOR FILING DATE: 1996-04-19 PRIOR APPLICATION NUMBER: US 08, PRIOR FILING DATE: 1997-04-18 NUMBER OF SEQ ID NOS: 130 SOFTWARE: PatentIn Ver: 2.0
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Schwab, George E.
Michaels, Tracy E.
Finstad Lee, Stacy
Burmeister, Paula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schnepf, H. Ernest
Knuth, Mark
                                                                                                                                                               Query Match
Best Local Similarity 47.0%;
Matches 131; Conservative
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4739 base pairs
                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                          448..4509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-378-088A-85
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                                                      TOPOLOGY: FEATURE:
                                                                                         ; NAME/KEY:
; LOCATION:
US-08-685-871-1
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APPLICANT:
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APPLICANT:
   LENGIH:
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APPLICANT:
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                       Gaps
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   Pred. No. 0.0039;
11; Mismatches 167; Indels
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Patent No. 6013499
GENERAL INFORMATION:
APPLICANT: NARUMIYA, Shuh
APPLICANT: IMAMATSU, Akihiro
TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1103 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1069
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3000 K Street, N.W., Suite 500
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION NUMBER: 28/08/685,871
FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-262553
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
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                       Conservative 211;
   4.38;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Washington
STATE: D.C.
   Best Local Similarity
Matches 17; Conserv
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US-08-685-871-1
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                                                                                                                                                                              627 ATATCCAGATGGTCAAACAATTGATGAGGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
                                                                                                                                                                                                                798 AGGTACAGATGAAATAAAAACACAACTAAATGAAGAATTAAAAATAGAATATAGTCATGA 857
                                              507 GAAAAIGIATIATATIGATICGGGAAAAGAAGAGIAGACGAGIACGATIAIGAIGCITC
                                                                                                567 TACATTATCCATCAGCAATCAACGGCCATTATTTACTTTTGAAAAGCATGAAGTGCCTGG
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0.36;
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Pred. No. 0.36;
0; Mismatches 152; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/378,088A CURRENT FILING DAFE: 1999-08-20 PRIOR APPLICATION NUMBER: US 08/633,993 PRIOR FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dojillo, Joanna
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA703C2
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42, Application US/09378088A
Patent No. 6372480
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Cardineau, Guy A.
Schwab, George E.
Michaels, Tracy E.
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Schnepf, H. Ernest
Knuth, Mark
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Best Local Similarity 45.5%;
Matches 127; Conservative (
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Burmeister, Paula
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PRIOR FILING DATE: 1997-04-1
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN VET. 2.0
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US-09-378-088A-42
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                                                                                                    567 TACATTATCCATCAGCAATCAACGGCCATTATTTACTTTTGAAAAGCATGAAGTGCCTGG
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Pred. No. 0.35;
0; Mismatches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Cardineau, Guy
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/633,993
FILING DATE: 1996
CLASSIFICATION: 435
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APPLICATION NUMBER: US/08/844,188
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Seguence 42, Application US/08844188 Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SANGERS, JAY M.
REGISTRATION NUMBER: 93.355
REFERENCE/DOCKET NUMBER: MA-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-375-800
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Best Local Similarity 45.5
Matches 127; Conservative
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STRANDEDNESS: single
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APPLICANT: Narva,
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ZIP: 32606-6669
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447 AAAAATGCACGAGGAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAA
                                         1401 AAAATATCAATATTGGCAACGAGCAGTAGGAAGTAATGTAGCTTTACGTCCACATGAAAA
                                                                                507 GAAAATGTATTATTTGGGGGAAAAGAAGAGGTAGACGAGTACGATTATGATGCTTC
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Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMBER: US 08/633,993
1996-04-19
TUMBER: US 08/844,188
1997-04-18
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/ENTION: Pesticidal Proteins
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Schnepf, H. Ernest
Knuth, Mark
Pollard, Michael R.
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Burmeister, Paula
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Matches 127; Conservative
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PRIOR FILING DATE: 1996-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-0
NUMBER OF SEQ ID NOS: 130
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        AAAATATCAATATTGGCAACGAGGAGTAGGAAGTAATGTAGCTTTACGTCCACATGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Saliwanchik, Lloyd & Saliwanchik
: 2421 N.W. 41st Street, Suite A-1
Gainesville
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APPLICANT: Schnepf, H. Ernest
APPLICANT: Routh, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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FILING DATE: 19-APR-1996
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/08844188 Patent No. 6127180 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2132 base pairs
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Best Local Similarity 45.5
Matches 127; Conservative
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PRIOR APPLICATION DATA:
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NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ IDSO
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LOCATION: 88050. 88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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INFORMATION: polymorphic fragment 5-124-273
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OTHER INFORMATION: polymorphic fragment 5-124-273
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               NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357
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INFORMATION: 5-148-352
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OTHER INFORMATION: 5-140-348
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LOCATION: 134374
OTHER INFORMATION: 5-140-361
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OTHER INFORMATION: 5-140-120
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OTHER INFORMATION: 5-145-24
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LOCATION: 146345
OTHER INFORMATION:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEEC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AN POLLET ACID MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE REPERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SEQ ID NOS: 140
SEQ ID NO 1
LENGTH: 162450
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                                                                                      Sequence 1, Application US/09345882
Patent No. 6399373
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OTHER INFORMATION: 99-1442-224
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OTHER INFORMATION: 99-1437-325
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LOCATION: 108149
OTHER INFORMATION: 5-135-198
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OTHER INFORMATION: 5-129-144
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OTHER INFORMATION: 5-130-257
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OTHER INFORMATION: 5-131-395
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OTHER INFORMATION: 5-135-155
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OTHER INFORMATION: 5-128-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 88073
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158 AAGTAGATAAACTGGTTTCTTTCATTATTCCCCTTGCT 195
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                                                                                          RESULT 9
US-09-434-408-3
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                                         OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
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LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEO ID36
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
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                                                                                                              SEQ ID33
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INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                               SEQ ID54
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Pred. No. 5.3;
0; Mismatches 77;
                                                                                                                                              NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144
FEATURE:
                                                                                                                                                                                                                                                                                                  ON: 99075..99121
INFORMATION: polymorphic fragment 5-130-257
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: polymorphic fragment 5-130-276
                                                                                                              INFORMATION: polymorphic fragment 5-129-144
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Best Local Similarity 51.3%;
Matches 81; Conservative
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NAME/KEY: allele
LOCATION: 108084..108130
       allele
97099..97145
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950 INGAYGCNGARMGNCARMGNYINCARGARCARYINAARCARACNGARCARAAYAIHWSNW 1009
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3.6%; Score 33.6; DB 4; Length 2
Best Local Similarity 21.5%; Pred. No. 2;
Matches 113; Conservative 115; Mismatches 290; Indels
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Sequence 3. Application US/09434408
Patent No. 6440697
GENERAL INFORMATION:
APPLICANT: Venezia, Domenick
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
FILE REFERENCE: 98 41
CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-111-04
CURRENT FILING DATE: 1999-111-05
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2169
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LOCATION: (1)...(2169)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                               Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION IRRORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILLING DATE: 03-Dec-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 206: US-09-453-702B-206
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Pred. No. 7.
                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                             APPLICANT: Blattner, Frederick R.
                   Sequence 206, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                             Burland, Valer
Perna, Nicole T.
Plunkett, Guy
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STRANDEDNESS: double
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Best Local Similarity 45.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 53701-2113
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US-09-453-702B-206/c
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14891 15010 ATGAGGATAACATTTTTAAATTTTATTCATCCTGGTGGTTGAACAATGAGAAAAAATATG 14951 4890 GGAATATTCATAATTAATGATTACGTGAGTTTCCAATGGCTAATGGTATTGAATTTAATC 14831 ö 574 455 ACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAATGT 514 635 ATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAA 694 575 CCATCAGCAATCAACGCCCATTATTTACTTTTGAAAAGCATGAAAGTGCCTGGATATCCAG 515 ATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTAT 14950 GTGAACTTACATCGTCTAAGAATAGAGTAGAAAGGAAGCTGTTGTACAGTACTATTTAAT Gaps E. coli 0157 ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage Indels 6365723el Sequences of 3.6%; Score 33.6; DB 4; 45.7%; Pred. No. 7.2; tive 0; Mismatches 139; NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386 REFERENCE/DOCKET NUMBER: 960296.95017 APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION: <Unknown> TOPOLGGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 261:
US-09-453-702B-261 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA: ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION: sequence 261, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION: APPLICANT: Blattner, Frederick TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-5000 TELEFAX: (608) 251-9166 Nicole T. 14770 TAACGCAAAAAATTC 14755 INFORMATION FOR SEQ ID NO: 261: STRANDEDNESS: single 695 TTATTAAAATCAGTAC 710 TITLE OF INVENTION: NO. 6
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS Ouery Match Best Local Similarity 45.73 Matches 117; Conservative Perna, Ni Plunkett, Burland, CITY: Madison COUNTRY: US STATE: WI

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447 AAAAATGCACGAGAGCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTGAA 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1152;
                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,188
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44.9%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 152;
5: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                          APPLICALL:

FILING DATE:
FLIST BARBARE 435

CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/633,993

TILING DATE: 19-APR-1996

"TING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-703C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/09378088A Patent No. 6372480
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pollard, Michael R.
Cardineau, Guy A.
Schwab, George E.
Michaels, Tracy E.
Finstad Lee, Stacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-844-188-37
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 44.9'
Matches. 124; Conservative
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                                                                                 COUNTRY: USA
ZIP: 32606-6669.
COMPUTER READABLE FORM:
                                          Gainesville
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APPLICANT: Narva, h
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    ADDRESSEE:
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                                                                                        GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 CCTGGCCGTTTTGTAGTCAGTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTT
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                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.2;
Pred. No. 2;
                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schnepf, H. Ernest
APPLICANT: Knuth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Cardineau, Guy
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
                                               Sequence 244, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08844188
Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/OCKET NUMBER: PB3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Narva, Kenneth E.
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50.6%;
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REGISTRATION NUMBER: 36,
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Best Local Similarity 50.6'
Matches 80; Conservative
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STRANDEDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Narva,
                                                                                                                                                                                                                                                           STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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US-08-961-527-244
                                                                                                                                                                                                                                                                                               20850
                                US-08-961-527-244
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 1152;
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Pred. No. 2.7;
0; Mismatches 152; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGCGAATTATAAAATCAGTACCCAACAACCGGA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCAAAATAATGGAAAAATATCAGGAACAATCAGA 893
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2421 N.W. 41st Street, Suite A-1
              APPLICANT: DOJILO, JOANNA
TITLE OF INVENTION: Pesticidal Proteins
FILE REFERENCE: MA703C2
CURRENT APPLICATION NUMBER: US/09/378,088A
CURRENT FILING DATE: 1999-08-20
PRIOR PILING DATE: 1996-04-19
PRIOR FILING DATE: 1996-04-19
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Foulth, Mark
APPLICANT: Pollard, Michael R.
APPLICANT: Schwab, George E.
APPLICANT: Schwab, George E.
ATITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
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Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bacillus thuringiensis US-09-378-088A-37
                                                                                                                                                                                                                                                                                                                                                                                                            3.5%;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Burmeister,
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                              LENGTH: 1152
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                                                                                                                                                                                                                                                                      SEQ ID NO 37
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1575 AAAATATCAATATTGGCAACAAGCAGTAGGAAGTAATGTAGCTTTACGTCCGCATGAAAA 1634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627 ATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGG 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%; Score 32.8; DB 3; 18 Best Local Similarity 44.9%; Pred. No. 3.6; Matches 124; Conservative 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 ACAGCGAATTATTAAAATCAGTACCCAACAACGGA 722
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Job time: 74 secs
                                                                                                           NAME: Sanders, Jay M. REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-703C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ 1D NO: 34:
  US 08/633,993
                          19-APR-1996
                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      2230 base pairs
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pair
                                                                                                                                                                                                                                                                                                                                                                                                single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-844-188:34
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C92366 C92366 C92366 Dict C92731 C92731 Dict C92540 C92540 Dict C92417 C92417 Dict														ALIGNMENTS	638 bp mRNA linear EST 08-APR-2002 ain Normalized Library, BB16 Apis mellifera 02 5', mRNA sequence.		honeybee. Apis mellifera Elskaryote, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;	Apriacy, April (Dases I to 638) Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L., Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E. Annotated expressed sequence tags and cDNA microarrays for studies	-566 (2002)	c	505 S. Goodwin Ave., Urbana, IL 61801, USA Tel: 217 265 0309 Fax: 217 244 3499 Email: generobi@life.uiuc.edu This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
1444	14 C	9 AIG 10 AV 13 BC	13 BJ 13 BJ 10 AV 13 BJ	13 B.	13 BJ 12 BC	13 89	13 8 8 8	13 B1 13 B1 9 AA	13 13 13 13 13	13 13 13 13 13	13 B.	12 AU	9 AI		Bee Bra	365300	oa; Art) erygota	38) Sand, M.E Srtson, B	1), 555	Robinson comology linois	re., Url ) ) Life.uil s fundec ives Fun
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655 655 655 655	65	64. 63. 62. 62.	62 61.4 61.2 61	60.2 59.6 59	59 58.6	57.4	57.4	57.4 57.4 56.6	56.2 56.2	55.4	. 4. v.	54.4	52.6 52		Z.	-	Σ			Col	505 (Tel: Tel: Fax: Email This Research
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: August 1, 2003, 12:07:04; Search time 1751 Seconds (without alignments) 8546.333 Million cell updates/sec	Title: US-10-089-986-1 Perfect score: 924 Sequence: 1 atggggccagttgttgaaaacgggagttaaagtgaagcta 924	able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 16154066 seqs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	ST:*		em_estmu				15: em_estfun:* 16: em_estom:* 17: 9D_gss:* 18: em_gss_in:*		24: em_gss_man: * 24: em_gss_nus: * 25: em_gss_other: * 27: em_gss_pro: *	rth sdr		Query Score Match Length DB ID	1 105.6 11.3 666 10 AV401529 BIS1828 BIS180016B 3 71.2 7.7 670 13 BIG11823 BIG11823 RH18245.5 4 66.4 7.2 635 13 BIG17530 BIG17530 RH47894.5 5 65.4 7.1 719 9 AJ425659 AJ425659 AJ425659 6 65.2 7.1 655 13 BIG17627 BIG17627 RH48022.5

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                                                                                                                                                                                                                                                                                                                          /note-"Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups."
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Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield
                                                                                                                                                                                                                /clone="BB160016B20002"
/clone="BB160016B20002"
/clone="BB60016B20002"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.6; DB 13; Length 638;
                                                                                                                                                                                 European bees,
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                                                                                                                                                                                                                                                                                           /dev_stage="adult worker honey bee"
/lab_host="DH10B"
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); Mismatches 299;
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                                                                BACKWARD: ATTAACCCTCACTAAAG
plate: BBL6010BBD row: D column: (
properties of the properties of the primer: Accordance acop: 638.
High quality sequence stop: 638.
                                                                                                                                                             /organism="Apis mellifera"
/strain="mixed strains of
A.m. ligustica"
/db_xref="taxon:7460"
                                   PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                               /tissue_type="brain"
                                                                                                                                     Location/Qualifiers
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Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmitu@inis.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                                     AV401529 Bombyx mori diapause-cancelled embryo p50 76 hr after HCl treatment (HCl at 20 hr after oviposition) Bombyx mori cDNA clone e96h0839 T3, mRNA sequence.

AV401529. GI:6905181
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hr after HCl treatment (HCl at 20 hr after oviposition)"
/sex="female/male mixed"
/tissue_type="diapause-cancelled embryo"
/dox_stage="76 hr after HCl treatment (HCl at 20 hr after
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (50->3')
Project-'Silkworm Genome Program in MAFF, and Research for
Future Program in JSPS'. see 'SilkBase',
chttp://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       Bombycoidea; Bombycota; Lepidoptera; Glossata; Ditryt Bombycoidea; Bombycoidea; Bombycoidea; Bombyx.

1 (bases 1 to 666)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Bombyx mori cDNA
Unpublished (2000)
Contact M+...
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/clone="e96h0839"
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Similarity · 56.8%;
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TITLE
JOURNAL
COMMENT
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                                                                                                         RESULT 2
AV401529
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Db 273 GATGCGTTTCGTACGGTCATCGTCCGGGATGGAGTCTCCGCAGTGGCCAAGGTCA 332  Qy 281 TAGAAGCTATTGTTAATGTCGAACCACATATAAAATAAA	OY 341 CAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAG 400 1	450 cccaatggaagggtgagctctacagctggcagggccggtgacagcctartcgta 461 gcaacatagctatagcaaatgggctcgggtggagtaatgaattgaagaaatgtattata 111	Qy         521 TTGATTCGGGGAAAGAAGAAGAAGAAGAACGATTATGATGTTCTACATTATCCATCA 580           b	RESULT 4 B1617530 LOCUS B1617530 B1617530 DEFINITION RH47894.5prime RH Drosophila melanogaster normalized Head pFlc-1 DFFINITION RH47894 Sprime RH Drosophila melanogaster cDNA clone RH47894 5 similar to regucal cin.	•	AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farian,D., Frise,E., George, J., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.  TITLE BDGP/HHMI RH Drosophila EST Project JOURNAL Unpublished (2001) Contact: Stapleton, M. BDGP	Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003706: arm:3R [10470528,10725488] estimated-cyto:88D2-88E1: 08/18/2001 Plate: RH.478 row: H column: 10 High quality sequence stop: 528. FEATURES Location/Qualifiers	ע
340 GCAGATCCCCTTGGCAATCTATGGACAGGTACTGACGCTGGTC 391		B1611823 B1611823.1 G1:15507348 EST. fruit fly. f Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Ephydroidea; Drosophilidae; Drosophila.  I (bases 1 to 670) Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,R., Gonzalez,M., Guarlin,H., Harris,N., Li,P., Liao,G., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,		Fax: 510 Email: ht hit genom estimated Plate: RH High qual	166 a	Similari 3; Cons TTGGAGF 	107 AGAAACTTTCATAAATGTACCTTCTCAGAAAAATACAGGTTTGTAAAG 160
OY Db RESULT 3	BI611823 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT	FEATURES	BASE COUNT	ORIGIN  Query Match Best Local Matches 27  Qy 47  Db 93	0y 0y 0y

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BIG17627
RH48022.Sprime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster cDNA clone RH48022 5 similar to regucalcin:
FBan0001803 GO:[] located on: x llA3-11A4;: 08/18/2001, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 AGCTTGACGACAGTTCTTTNGACAAAAGTTTAGTTAATGGGCACGTCTACAGAGTAACAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643
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                                                                                                                                                                                                                                                                                                          TCACTGGCAGTT---TATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGAGCA 463
                                                                                                                                                                                                                                                                                                                                                                               148 TGAAGCAGGGTTCTCTGTTCTCCCTGAACAAGGACCACATTGTAGTCAAACATTTCAATC 207
                                                                                                                                                                                                                                                                                                                                                                                                           ACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                         267
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/tissue_type="spleen"
/tissue_type="adult"
/dev_stage="adult"
/note="Vector: Stratagene lambda Uni-Zap; country=United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTGGACATCTCAAACGGTCTGGACTGGTCTCTGGACCACAAAACCTTCTACTACATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGTACCCAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 ATCAACGGCCATTATTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAA
                                                                                                                                                                                                                                  287 CTATTGTTAATGTCGAACCACACTTAAAAATAACAGACTCAATGATGGCAAAGCAGATC
                                                                                                                                                                                                                                                    347 CCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAGGACCGG
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                      13;
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                                                                                                                                                                                                      Indels
                                                                                                                                1 others
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                                                                                                                                                                       Score 65.4; DB 9;
Pred. No. 2e-07;
0; Mismatches 322;
                                                                                                                                u
                                                                                                                                161
            /organism="Salmo salar"
/db_xref="taxon:8030"
/clone="$20006"
                                                                                                                                 9
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Drosophila melanogaster
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al Similarity 47.3%;
301; Conservative
                                                                                                                                   168 c
                                                                                                                     Kingdom"
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                                                                                                                                                                                                                                                                                                                                                340
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                                                                                                                                                   47 TTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAG 106
                                                                                                                                                                     160
                                                                                                                                                                                                                                                                     TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA 220
                                                                                                                                                                                                                                                                                                                               GTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTTAGTGCTGCACCTACAAGCA 280
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BamHI: Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                         281 TAGAAGCTATTGTTAATGTCGAACCACATTAAAAATAACAGACTCAATGATGGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATATA
                                                                                                                                                                                                            AGAAAACTTTTCATAAATATGTACCTTCTCAGAAAAAATACACGTTTTGTAAA-----G
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                                                                                          Length 635;
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                                                                                         Score 66.4; DB 13;
Pred. No. 1e-07;
0; Mismatches 276;
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Institute of Aquaculture
University of Stirling
Airthrey Road, FK9 4LA, U
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                                                                                            7.28;
                                                                                                                        Conservative
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Salmo salar
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                                                                                                             Similarity
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                                                                                                                          Matches 261;
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                                                                                             Query Match
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AJ425659
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C92366 560 bp mRNA linear EST 12-JUL-1999 C92366 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cDNA clone SSE652, mRNA·sequence.
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1 (bases 1 to 560)

Morlo,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takenoto,K., Yasukawa,H., Williams,J., Maeda,M., Takenchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651
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510 GCAAGGTGGGCATATCCAATGGCCTGGCCTGAGATGTCAAGGCCAAGAAGTTCTACTTCA 569
                                                                                            570 TCGACACCAACAACCACGAGGTATTGGCCTATGACTACAATCAGAGCACCGGCGCCGTAA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:44689"
/clone="SSE652"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATATATTGATTCGGGG
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                                                TTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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Tel: 81-298-53-4664
Fax: 81-298-53-6614
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Pred. No. 2.4e-07;
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99156227
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83 c 104 g
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Dictyostelium discoideum
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50.48;
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                                                             (Asses 1 to 655)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
Stapleton, M., Gravez, C., Dorsett, V., Farfan, D., Frise, E., George
, R., Gonzalez, M., Gharin, H., Harris, N., Li, P., Liao, G., Misra, S.,
Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 TGGGCGAGGGACCCCACTGGGATGTTGATCGCCAGAGTCTGTACTACGTGGACCTCGAAT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAAACTTTTCATAAATATGTACCTTCTCAGAAAAAATACACGTTTTGTAAA-----G 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCCGCCGCTTAATCGTTTCAAGCAGAACAAAGTGTACAGGCCTAAAATCGAGG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTTAGTGCTGCACCTACAAGCA 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 CAGAȚCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/lab_host="DH5-alpha TonA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 TAGAAGCIATIGITAATGICGAACCACACATTAAAAATAACAGACTCAATGATGGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
                                                                                                                                                                                                                                                                                                                                     Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 4606 Rd, Berkeley, CA 94720, USA
Fax: 510 4406 Rd, Bruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003487: arm:X [11484037,11785087]
estimated-cyto:1004-111A4: 08/18/2001
estimated-cyto:1004-111A4: 08/18/2001
High quality sequence stop: 538.
Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH48022"
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Pred. No. 2.2e-07;
0; Mismatches 278;
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                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Stapleton, M.
BDGP
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Best Local S:
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C92540 tinear EST 12-JUL-1999 C92540 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cDNA clone SSE589, mRNA sequence.
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Dictyostellum discoideum.

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Dictyostellum discoideum

(bases 1 to 639)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Soshino, F., Mitra, B.N., Pil, M., Sato, T., Takemoto, K., Yasuakawa, H., Williams, J., Maeda, M., Takeuchi, I., Cochiai, H. and Tanaka, Y.

The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
378 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 437
                                                                 /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 GAGGAGGGTAATTTTATGGGTTGCCGTTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTTGATTCGGGG
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                                          772 GCATTIGGCGGTCCGAATTIGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hideko@biol.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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Pred. No. 2.5e-07;
0; Mismatches 180; Indels
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Tel: 81-298-53-4664

    639
    /organism="Dictyostellum discoldeum"

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University of Tsukuba
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99156227
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87 c 120
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Best Local Similarity 50.4%;
Matches 186; Conservative (
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C92540.1 GI:3074416
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 606)

Morlo, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshido, T., Mizuno, H., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostellum developmental cDNA project; generation and analysis of expressed sequence tags from the first-finger stage of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        712 CAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 GAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC 711
                                                                        GCATTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGAC 831
            ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
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Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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9915627
Contact: Hideko Urushihara
Institute of Bulogical Sciences
University of Tsukuba
1-1-1 Tennoudal, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
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Pred. No. 2.5e-07;
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/clone="SSF142"
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86 c 119
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Dictyostelium discoideum
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387 ATCACTAAAAAACTTTTATTAACTGTAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 446	Db 430 ATCACTAAAAACTTTTATAACTGTACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT 489
772 GCATITGGCGGTCCGAATITGGATGAACTGCAACATCTGCTGGTCTTCAGCTTGAC 831 	OY 772 GCATTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGAC 831   1   1   1   1   1   1   1   1   1
832 GACAGITCT 840           507 CCTGAITCT 515	Qy 832 GACAGTTCT 840           Db 550 CCTGATTCT 558
C92417 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum SS (H.Urushihara) Dictyostelium C92417.1 GI:3074293 EST. C92417.1 GI:3074293 EST. Dictyostelium discoideum. Willians, J., Maeda, M., Takemoto, R., Yasukawa, H., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, R., Yasukawa, H., Yoshino, R., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. Willians, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, T. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of Gevelopment. DNA Res. 5 (6), 335-340 (1998) 99156227 Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba I-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan	RESULT 11 C90258 LOCUS LOCUS LOCUS DEFINITION C90258 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium ACCESSION C90258 C90258 C90258 C90258 C90258 C90258 C90258 C90258 VERSION C90258
81-298-53-6614 1: hidekc@biol.tsukuba.ac.jp SCT = 'Dictyostelium discoideum No. Location/Qualifiers 1. 679 /organism="Dictyostelium d /strain="AX4" /db_xref="taxon:44689" /clone="SSE888" /clone="SSE888" /clone="Lib="Dictyostelium /dev_stage="slug"	rce 1730 /organism="Dictyostellum dis/strain="Axxv" /strain="Axxv" /db_xref="taxxv" /clone="SSI507" /clone=lib="Dictyostellum di/dev_stage="slug" /rcore 105 a 101 c 135 g 231 t /rcore 105 a 101 c 135 g 231 t /rcore 105 a 101 c 135 g 231 t /rcore 105 a 101 c 135 g 231 t /rcore 105 a 101 c 135 g 231 t
g 206 t re 65; DB 14; Length 679; 3. No. 2.6e-07; wismatches 180; Indels 3.	Conservative ( ATAGCAAATGGGCTCGCGTC
ATAGCAAATGGGCTCGCGTGGAGTAATGATTGAAGAAAATGTATTATATTGTTCGGGG 53  ATAGCAAATGGGTAGGTAATGATTGATTGAAAAATGTTTATTATT	Qy         532 AAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAAGG         591           I           1   1
592 CCATTIOAATACCATGAAATGGATTACAACGCTGCCCAAGGCACTGTATCAAATGGT 312 592 CCATTATTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAAGGCAATGGT 651 1	Qy         652 GAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCAATTATTAAAATCAGTACC 711           Db         430 AGTGAAGTTACTGGATTGCTCATTGGGAGGGTGGTACAGATGGTGCTCCA         489           Qy         712 CAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTA         771           Db         490 ATCACTAAAAAAATTGATAACTGTTACAAATGTCTCAAAGGTCACTTCTGT         549           Qy         772 GCATTTGGCGGTCCGAATTTGGATGAACTGTTCCAAATGTCTCAAGGGTCACTTCTTGT         549           PI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                     BJ435579 Tictyostelium discoideum cDNA linear EST 13-MAR-20
BJ435579 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv27g15 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase" 2 others
137 c 104 g 265 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 GAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAAAATGTATTATATTGATTCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 CCATTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGAT
                                                                                                                                                                                                                   Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

[ Loases 1 to 743)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 2.6e-07;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill1 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="AX4"
/db_xref="taxon:44689"
/clone="ddv27g15"
                                                                                                                                                                                                                                                                                                                                                                                             tshini@genes.nig.ac.jp.
Location/Qualifiers
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Dictyostelium discoideum
                                                                                                                                                               BJ435579.1 GI:19410301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.0%;
Best Local Similarity 50.4%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         832 GACAGTTCT 840
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      832 GACAGTTCT 840
                                 CCTGATTCT 618
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/dev_stage="adult"
/lab_host="blidg"
/lab_host="blidg"
/note="corgan: liver; Vector: pME18S-FL3; Site_1: DrallI
/note="Corgan: liver; Vector: pME18S-FL3; Site_1: DrallI
(CACTGTGTG); Site_2: DrallI (ACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
was primed with an oligo(dT) primer
[ATGGGCTATTGT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCTATGTG], digested
and cloned into distinct DrallI sites of the pWE18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACTCCAGCACACA.

2 others
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                                 EST 10-MAY-1999
                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 555)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
Y. B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
'E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
555 bp mRNA linear EST 10-MAY-1999. ui999h04.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890583 5' similar to SW:SM30_MOUSE Q64374 SENESCENCE MARKER AL6676484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:974907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other_ESTs: ui99h04.x1
Other_ESTs: ui99h04.x1
Contact: Marra Mywashu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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49.5%; Pred. No. 3.6e-07;
tive 0; Mismatches 247; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 460. Location/Qualifiers
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:1890583"
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AI663645.1 GI:4767228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 513)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Ax4" / /strain="Ax4" /db_xref="taxon:44689" /clone="ddc10c20" /clone_"blctyostelium discoideum cDNA library, CF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGG
                                                                                                                                                                                                                                                                                                               GAGGAGGGTAATTTATGGGTTGC----CGTTTTCCAAGGACAGCGAATTATTAAAATCAGT
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   ATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGG
                      AAAAGAAGAAGAAGAAGATACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGG
                                                                                                                                              CCATTATTTACTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGAT
                                                                                                                                                                                                                                                                                        ACCCAACAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCT
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.8%; Score 62.4; DB 13;
Best Local Similarity 50.9%; Pred. No. 1.3e-06;
Matches 175; Conservative 0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Culmination stage"
103 c 82 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Dictyostelium discoideum
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BJ371993.1 GI:19281376
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1 (bases 1 to 730)
Satoh, N., Satou, Y., Rohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
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                                                                                               183 TTTGGATTGGTCCCTGGACCATAAAATCTTCTACATTGACAGCCTGTCCTACACTGT
                                                                                                                                                                                                                                      543 AGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCATTATTTAC
                                                                                                                                                                                                               603 TTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATGAGGAGGGTAA
                                                                                                                                                                                                                                                                                    663 ITTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAACAACGGA
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TCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGGAGCAACATAGCTATAGCAAATGG
                               123 CTCCCTCTTTCCTGATCACAGTGTGAAGAAATACTTTGACCAAGTGGATATCTCCAATGG
                                                                   483 GCTCGCGTGGAGTAATGATTTGAAGAAATGTATTATATTGATTCGGGGAAAAGAAGAGT
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Pred. No. 7.5e-07;
0; Mismatches 181; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ciona intestinalis"
/db_xxef="texon:7719"
/clone="rcic128p05"
/clone_lib="Nori Satoh unpublished
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/note="Vector: pBluescript SK"
166 c 134 g 233 t
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                 783 TCCGAATTTGGATGAACTGCATGTAACATCTGC
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ilarity 52.6%;
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Perfect score:

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Scoring table:

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B thuringiensis 58
B. thuringiensis 1
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Human digestive sy
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Nucleic acid encod
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/transl_except= (pos:782..784, aa:Leu)
/note= "No start or stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Firefly luciferin regenerating protein coding sequence.
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ABQ58878
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ABL59542
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AAS46741
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ABQ70703
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AAF86444 standard; DNA; 865
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                                     Firefly luciferin
Luciola lateralis
Nucleotide sequenc
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Rat regucalcin cDN
Mouse SMP30 encodi
Human SMP30 gene.
Senescence marker
Gene #1648 used to
                                                                                                                             August 1, 2003, 12:01:21; Search time 292 Seconds (without alignments) 7126.186 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAQ90035
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Kajiyama N;

Kurosawa K,

Query Match I

Score

NO.

Result

is

Pred. No.

35.2 34.7 10.7 9.8 8.7 8.1 8.1 9 6

325.2 320.4 98.6 90.4 80.8 74.4 74.4

us-10-089-986-1.rng

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Sequence 924 BP; 325 A; 146 C; 178 G;
                                                                         TTCCCGGGAGTTAAAGTGAAGCTA 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 17-18; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                          TTCGCGGGGGTTAAAGTGAAGCTA
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556; Conservative
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                                                                                                                                                                  DNA;
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B; ABB06339.
                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the coding sequence from firefly for a protein that regenerates luciferin by using oxyluciferin and D-cysteine. The encoded protein can be used for regeneration of luciferin, a substrate for luciferase, used for ATP (adenosine triphosphate) assays in both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGTGTTACTGGATACCGTAAAATACCAGATCCTCAGGTCACCTCTGTAGCATTTGGC
                                                                                                                                                                                                                                                                                                                                                                                  GGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAAAGAAGA
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                                                            protein and gene encoding it useful for luciferin from oxyluciferin and D-cysteine
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                                                                                                                                                                                                                                                              Length 865;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                Sequence 865 BP; 267 A; 163 C; 195 G; 239 T; 1 other;
                                                                                                                                                                                                                                                              Score 863; DB 22; I; Pred. No. 3.1e-242; 0; Mismatches 0;
                                                                                                           21pp; Japanese
                                                                                                                                                                                                      medical and food hygiene areas.
                                                                                                                                                                                                                                                                93.4%; ; 100.0%;
                                                                                                                                                                                                                                                                                             864; Conservative
                                                                                                            Page 14-15;
                                                                Luciferin regenerating regenerating expensive
                   2001-266307/27
                                                                                                                                                                                                                                                                                Similarity
                                   P-PSDB; AAB82087
                                                                                                              Disclosure;
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Luciola lateralis-originated genes encoding proteins capable of regenerating luciferin especially from oxyluciferin, useful for producing recombinant DNAs and transformants to give proteins useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a protein capable of regenerating luciferin, which is isolated from Luciola lateralis (Japanese firefly). The gene encoding the protein capable of regenerating luciferin can be used for producting recombinant DNAs and transformants, which can be used for the production of proteins useful in assaying adenosine triphosphate (ATP) in medical sciences and food hygiene. The protein can be added to the luciferin-luciferase reaction system to sustain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGGGCCAGTTGTTGAAAAATTGCAGAACTTGGCAAGTATACGGTTGGAGAAGGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luciola lateralis; luciferin; regeneration; Japanese firefly; adenosine triphosphate; ATP; medical science; food hygiene; luciferase; luminescence; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Luciferin regeneration protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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60.2%; Pred. No. 8.2e-85;
cive 0; Mismatches 364;
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26-JUL-2001;
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                                                               07-FEB-2002
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                AAATATGTACCTTCTCAGAAAAAATACACGTTTTGTAAAGTAGATAAACTGGTTTCTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luciferin. The protein can especially regenerate luciferen from oxyluciferin. The protein can be added to the luciferin-luciferase reaction system to sustain luminescence and reduce the amounts used. The polynucleotide sequence is useful for producing recombinant transformants, which are useful for the production of proteins useful in assaying ATP in medical sciences and food hygiene.
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                                                                    "Luciferin regenerating protein"
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Pred. No. 2.1e-83;
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Location/Qualifiers
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         TCCAATGGTCTTGCAGTAAAGATTTAAAAAAGTTTTATTACATTGATTCTGCTGTT
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                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 32981
                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                               cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB77072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                   47 TTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AGAAAACTITTCATAAATATGTACCTTCTCAGAAAAAATACACGTTTTGTAAA-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
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                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                  912;
                                                                                                                                                                                                                                                                             Score 98.6; DB 23; Length
Pred. No. 1.7e-18;
0; Mismatches 379; Indels
                                                                                                                                                                                                                                Sequence 912 BP; 231 A; 246 C; 238 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                  10.7%;
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us-10-089-986-1.rng

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946
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                                                                                                                                                                                               894
655 GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-human animals with defective senescence marker protein 30 function, useful for producing antibody, histopathological diagnosis and onset mechanism of disease due to aging, and in screening side-effects during
                      SMP30;
                                                              715 CAACCGGAAGTGTTACTGGATACCGTAAAAATACCAGATCCTCAGGTCACCTCTGTAGCA
                                                                                   775 TITGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
                                                                                                                                                             827 TTTGGAGGGAAGGATTACTCTGAAATGTACGTGACATGTGCCAGGGATGGGATGAGCGCC
                                                                                                                                                                                              835 AGTICTITNGACAAAAGTITAGTIAAIGGGCACGICTACAGAGTAACAGGTITAGGCGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; senescence marker protein 30; cancer; aging; senescence; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1573 BP; 453 A; 288 C; 366 G; 466 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 38-40; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse SMP30 encoding cDNA SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
73..972
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                            ABL99968 standard; cDNA; 1573
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/product= '
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P-PSDB; ABB83787.
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(KASA/) KASAHARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                             ABL99968;
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ABL99968
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L. 33388 was isolated and sequenced (AAQ87295). The protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding regucalcin - useful for the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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aa:His
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Pred. No. 4.9e-16;
0; Mismatches 292;
                                                                                                                                                                                                                                                                            /transl_except= pos:362..364,
/transl_except= pos:500..502,
                                                                                                                                              ds.
                                                                                                                                           Calcium binding protein; regucalcin; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regucalcin, a calcium binding protein
                                                                                                                                                                                                                                                           /product- regucalcin
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DAII-) DAIICHI KAKAGU YAKUHIN KK.
(YAMA/) YAMAGUCHI M.
               BP.
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             CDNA; 1216
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Best Local Similarity 50.2°
Matches 307; Conservative
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/*tag=
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                                                                                                            Rat regucalcin cDNA
           AAQ87295 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR75416.
                                                                                                                                                                           Rattus rattus
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                               GTCGAACCACATTAAAAATAACAGACTCAATGATGGCAAAGCAGATCCCCTTGGCAAT 357
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                                                                                                            469 TCCTTGTACTCCCTCTTTCCTGATCACTGTGAAGAAATACTTTGACCAAGTGGATATC
                                                                                                                                       535 AGAAGAGTAGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                             GTGGATGAAGATAAGAAAAATAATCGATTCAATGATGTGGAAGGTGGATCCTGCTGGGAG
                                                               358 CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTA---GGACCGGTCACTGGC
                                                                        409 TACTITGCTGGTACCATGGCTGAGGAAACGGCCCCAGCTGTTCTTGAGCGCCCAAGGG
                                                                                               AGTITIATATCATITAGGGGCTGATAAAAGGTAAAAATGCACGAGAGCAACATAGCTATA
                 Gaps
                12;
 Length 1573;
                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMP30; marker protein; ageing; organ development;
 Score 80.8; DB 24;
Pred. No. 3.6e-13;
); Mismatches 298;
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/product= SMP30 marker protein
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                                                                                                                                                                                                                                                                                                                                                                                                           mRNA; 1356
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94..993
/*tag= a
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  8.7%;
49.3%;
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                   301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            AAQ90035 standard; cDNA
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|AAAGGAATTGC
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SMP30 gene.
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     Query Match
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Matches 3(
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GAGGGTCTTTTGAGGCAACCTGAAGCTGGAATTTTCAAGATAACTGGTCGGGGGTC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549
                                                                                                                                                                                                                                                                                                      AAQ90035 is the SMP30 gene. It encodes the human ageing marker protein, SMP30 (AAR74219). Human SMP30 is found in human organs, tissues, blood, urine and cerebrospinal fluid. The blood concentration of SMP30 is known to increase with renal and hepatic deficiencies and to decrease with age. It is therefore useful in the monitoring of renal or hepatic deficiencies and for the monitoring of the development of the liver and kidneys in newborn babies.
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                                                                                                                                                                              Novel polypeptide for detecting human ageing marker protein SMP30 for monitoring liver and kidney development in new-born bables
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.4; DB 16; Length 1356;
Pred. No. 2.5e-11;
0; Mismatches 302; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1356 BP; 373 A; 274 C; 343 G; 366 T; 0 other;
                                                                                                                                                                                                                                                                    Claim 3; Page 6-7; 10pp; Japanese.
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Best Local Similarity 48.6%;
Matches 297; Conservative
93JP-0265681
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P-PSDB; AAR74219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCAATTATTAAAATCAGTACCCAA
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                                                              GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
                                                                                                                                          535 AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                                                                                                                                                  610 TACTCCGTGGATGCCTTTGACTATGACCTGCAGACAGGACAGATCTCCAACCGCAGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1648; 298pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by an uclaic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                              Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obata Y, Old
, Stockert E;
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Scanlan MJ,
                                                                                                                                          Senescence marker protein SMP30 gene.
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                    BP
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AAX40196
ID AAX40196 standard; DNA; 1356
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97US-0896164
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chuh M, Sahin U,
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Best Local Similarity 48.6
Matches 297; Conservative
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26-MAR-2002 (first entry)

us-10-089-986-1.rng

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN3503-ABN9455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, or the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 2.5e-11;
); Mismatches 302; Indels 12;
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Matches 297; Conserv
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ABL12832/c ID ABL12832 standard; cDNA; 2970 BP.

RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                       NO 32978
                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70.4; DB 23; Length 2970;
Pred. No. 5.3e-10;
0; Mismatches 341; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                     Drosophila melanogaster expressed polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2970 BP; 893 A; 558 C; 574 G; 945 T; 0 other;
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                                                                                                                                                                                                                                                                                                                  EM
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320; Conservative
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                                                                                                          Drosophila melanogaster.
                                                           Drosophila; developmer
pharmaceutical; gene;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                       TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTACAAGGTTAATCCCAACACTGGCAAGATTCTGCTTGAGATC---AAGTTCCCAACCA
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                                                                                      Gaps
                                                                                    18;
                                           Length 1086;
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237 T; 0 other;
                                                                                    0; Mismatches 400;
                                        Score 67; DB 23;
Pred. No. 3.3e-09;
C; 296 G;
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245 A; 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                             GCAACATAGCTATAGCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATA
                        GCAATCAACGGCCATTATTTACTTTTGAAAAGCAT-----GAAGTGCCTGGATATCCAG
                                                                                                                                                                                                                                ATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAA
                                                                          TTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                            insecticide;
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0; Mismatches 400; Indels
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                            developmental biology; cell signalling;
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genes from Drosophila and
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Best Local Similarity 46.6
Matches 365; Conservative
                                                                                    Drosophila melanogaster
                          Drosophila; developmer pharmaceutical; gene;
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                                                                                                                           224 CAGGCAGCCTGCTCCGCTACGACTATGCGCAGAACAAGGTCTACAAGACAAAGATCGAGG
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                                                                      7.3%; Score 67; DB 23; Length 1119; llarity 46.6%; Pred. No. 3.3e-09; Conservative 0; Mismatches 400; Indels 16
                                                   Sequence 1119 BP; 266 A; 302 C; 310 G; 241 T; 0 other;
(ABB57737-ABB72072).
The sequence data for this patent did not form part o specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 AGAAAACTTTTCATAAATATGTACCTTCTCAGAAAA-----AATACACGTTTTGTAAAG
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                                                                                                                  developmental biology; cell signalling; insecticide;
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16.0%; Pred. No. 8.2e-05;
tve 0; Mismatches 337;
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11-JUL-2000; 2000US-0614150.
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ABL03468 standard; cDNA; 3554 BP.

RESULT 14 ABL03468 ID ABL0 XX AC ABL0

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                                                                            2019 TCGATACCACCGACTACGAGGTGAAGTCGTATGACTATGATTTCGAGACCGGCGTGGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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pharmaceutical; gene;
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P-PSDB; ABB59363.
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Length 4624;
                                                                                 Indels
Score 52.8; DB 23;
Pred. No. 9.3e-05;
); Mismatches 337;
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0
    5.7%;
        Query Match
Best Local Similarity 46.0
Matches 300; Conservative
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completed: August 1, 2003, 12:06:43 ne : 305 secs Search co

Sequence 4624 BP; 1242 A; 1013 C; 1017 G; 1352 T; 0 other;

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August 1, 2003, 12:01:54; Search time 2636 Seconds (without alignments) 10201.439 Million cell updates/sec
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924
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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AB072447 Luciola 1
AB072448 Luciola c
AY07130 Drosophil
AY028616 Calliphor
AB023450 Drosophil
E09237 CDNA insert AB037936 Xenopus 1 AX409001 Sequence E09013 cDNA encodi D31815 Human mRNA AB028125 Homo sapi AB032064 Homo sapi AB03306 Xenopus 1 AP000987 Sulfolobu AB03346 Bos tauru AC013939 Drosophil AE007808 Brosophil U05664 Sulfolobus
AB03445 Oryctolag
AY118643 Drosophil
AC115963 Dictyoste
AB079885 Sarcophag
AE006864 Sulfolobu
AP009990 Sulfolobu
AP077935 Gallus ga
AC014187 Drosophil AC014187 Drosophil AC023688 Drosophil AE0063487 Drosophil AC023731 Drosophil AX083744 Sequence AP005199 Oryza sat I66494 Sequence 14 AB062786 927 bp mRNA linear INV 27-SEP-200 Photinus pyralis mRNA for luciferin regenerating enzyme, complete E09237 cDNA insert AB036903 Sarcophag score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Photinus pyralis cDNA to mRNA. Photinus pyralis Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Photinus. Description ALIGNMENTS SUMMARIES RNSMP30A AB037934 D86217 AY071130 AY028616 AB029490 AF326959 E09237 AB036903 MMU28937 AC014187 AC023688 AX409001 E09013 HUMSMP30 AB033368 AB035446 AB079885 SAU05664 AP000990 RATCBP1 AB032064 AP000987 AB062786 AB062786.1 GI:14331151 Gomi, K. and Kajiyama, N. 2 DB 1438 1088 269050 1394 49817 167195 254961 Query Match Length 1216 1155 11594 1594 1605 1109 1573 888 1357 1108 633 10105 164237 7218 56152 286756 76808 7 186714 7 301051 AB062786 923 325.2 320.4 98.6 97.2 62.8 62.8 59.8 59.2 Score RESULT 1 AB062786 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS Result М О

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Aug

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NDNLWYAIVRGGKVINIGTRQPESLLGVINNPESLITSVCFGGSKLDELYVTTSGIKE
PETDSYRTKUKGGLYNTGLGVKGEDPARFSL"
146 c 178 g 275 t
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Gomi,K., Hirokawa,K. and Kajiyama,N.

Gomi,K., Hirokawa,K. and Kajiyama,N.

Submitted (04-0CT-2001) Keiko Gomi, Kikkoman Corporation, Research and Development Division; Noda 399, Noda, Chiba 2780037, Japan (E-mail:8553@mail.kikkoman.co.jp, Tel:81471235579, Fax:81471235550)
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Molecular cloning and expression of luciferin-regenerating (LRE) cDNA in Luciola cruciata and Luciola lateralis
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/protein_id="BAB85478.1"
/db_xref="G1:18857905"
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Pred. No. 1.1e-70;
); Mismatches 364;
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/db_xref="taxon:7052"
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SQKKYTFCKVDKLVSFIIPLAGSPGRFVVSLEREIALLTWDGVSAAPTSIEAIVNVEP
HIKNNRLNDGKADPLGNLWYGTMAIDAGLPVGPVTGSLYHLGADKKYKMHESNIAIAN
GLAMSNNLFKNYYIDSGKRYNDEYDYDASTLSISNQRPLFTFKHEVPGYPDGQTIDE
EGNLWAVAVEGGRIIKISTQQPEVLLDTVKTPDPQVTSVAFGGPNLDELHVTSAGLQL
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       is
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       luciferase,
                                                           (bases 1 to 927)

Channing and Kajiyama, N.

Direct Submission

Submitted (07-JUN-2001) Keiko Gomi, Kikkoman Corporation, & Development; Noda 399, Noda-shi, Chiba 2780037, Japan (E-mail:8553@mail.kikkoman.co.jp, Tel:81471235579)
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Pred. No. 3e-220;
0; Mismatches 1; Indels
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     firefly
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regenerated into luciferin
. 276 (39), 36508-36513 (2001)
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1. .927
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99.98;
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SOURCE Luciola cruciata CDNA to mRNA.  ORGANISM Luciola cruciata CDNA to mRNA.  ORGANISM Luciola cruciata CDNA to mRNA.  REPERENCE  RATHORS GOOM, X. HILOKAWA K. and Kajiyama, N.  TITLE  ANTHORS GOOM, In Luciola cruciata and Luciola lateralis  CADDECULA: HILOKAWA K. and Kajiyama, N.  TITLE  ANTHORS GOOM, In Luciola cruciata and Luciola lateralis  CLRB) CDNA in Luciola cruciata and Luciola lateralis  ANTHORS GOOM, K., HILOKAWA K. and Kajiyama, N.  ANTHORS GOOM, K., HILOKAWA K. and Kajiyama, N.  ANTHORS GOOM, R., HILOKAWA K. and Kajiyama, N.  COORIS GOOM, R., HILOKAWA K. and Kajiyama, N.  ANTHORS GOOM, R., HILOKAWA K. AND KALOKO GOOM, CHARLA ZBOOM, CHARLA GOOM, R., HILOFAWA K. AND K. A	GTTCCGATCTTTATTGTGAGTTTA TTAGTCCGACTACAGATGAA TTAGTCCTGCACACAGATAGAA TTAGTCTCCTCCAAGATAGAA AAAATACACTCAATGATGCCAAA AAAAAAAAGACTTAAATGACGTAAA TGGCTATTGACGTGGTCTCCCCGTA TGAAATGGTTCAGATCATCCCCGTA TGAATAGGTTCAGATCATCCCCGTA TGAATAGGTTCAGATCATCCCCGTA TGAATAAGCAAAAATGCACGGGTCTCATAAAAGCAAAAAGGTAAAAAGGTAAAAAGGTAAAAAGGTAAAAGGTAAAAGGAACGTGTCATAAAAGCAAGGTAAAAGGAACACGTGTAATAAGCAAGGTAAAAGAACACGTGTCATAATAAGCAAGTGAAAGAACACGTGTCTAATAAGCAAGTGAAAAGCAAGTGTAATAAAGCAAGTGAAAAGAACACGTGTCAATAAAGCAAGTGAAAAAGAACACGTGTCAATAAAGCAAACACGTGTCAATAAAACAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTAG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 GACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAATGCACGAGA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGGTGGGCATATCCAATGGCCTGGCCTGGGATGTCAAGGCCAAGAAGTTCTACTTCA 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TTGGAGAAGGTCCTCACTGGGATCATGAAACTCAGACCTTATATTTCGTCGACACCGTAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 CTCGCACCCTGTTCGAGGTGCAGCGGACCTGAAGGAAAACGGCCTTAATGATGACAAAA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCCGCCATTAATCGTTATGATTTCAAGCAGAACAAAGTGTACAGGGCTAAAATCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 TAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGTAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 GATGCGGTCTTCGTACGGTCATCGTCGGATGGAGTCTCCGCAGTGGCCAAGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                         /note="alignment with genomic scaffold AE003706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1040;
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Pred. No. 5.2e-14;
0; Mismatches 379; Indels
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    or
(http://fruitfly.berkeley.edu)
cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;

Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 1040)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., George, R., Gonzalez, M. (Barinh, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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                                                                                                                                                                                                                                                                         GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  835 AGTICTITNGACAAAAGITITAGITAAIGGGCACGICTACAGAGIAACAGGITIAGGCGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submission (18-DEC-2001) Berkeley Drosophila Genome Project, Submitted (18-DEC-2001) Berkeley, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY071130 1040 bp mRNA linear Drosophila melanogaster RE17477 full length cDNA. AY071130 AY071130.1 GI:17945393
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KEYWORDS
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Qy         161 TAGATAAACTGGTTTCATTATTCCCCTTGCTGGATCCCTGGCCGTTTTGTAGTCA         220           Db         205 GTGAGGATTTAGCTGTGCCCGTCGAAGGTACAACCGATCAATTGCTGTCG         264           Qy         221 GTTTGGAAGGTGAATAGCCATTCTTACATGGGATGGTCTGCACCTACAAGCA         280           II         III         IIII         IIII           Db         265 GTTCTGGTCGTCGTGGAACAATGGGATGGTGTTTCTGAGACCGCTAAAGTAT         324           Qy         281 TAGAAGCTATTGTAAATGTCGAACCACATTAAAAAT         311           Db         332 TGAAGACTTGTTCGAAGTGCAAACGGTGATGAAGGTTTCACTGCCAACGCTTCAATG         384           Qy         332 ATGGCAAAGCAGATCCGTTGGCAATCTATGGACGGTACAATGCTTTCACTGCCACCGTC         391           IIIIII         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	392 TCCCCGTAGGACCGGTCATGGCAFTTATATCATTTAGGGGCTGATAAAAAGGTAAAAA	RESULT 6 AB029490 LOCOUS DECOUSE DEFINITION COMPLETE CAS. ACCESSION NBD2940  ACCESSION NBD2940  ACCESSION NBD2940  ACCESSION NBD29400  ACCESSION NBD20400  ACCESSION N
QY         635 ATGGTCAAACAATTGATGAGGGGGAATTTATGGGTTGCCGGTTTTCCAAGGACAGCGAA 694           1 1	RESULT 5 AY028616 AY0	/product="anterior fat body protein" /product="anterior fat body protein" /product="anterior fat body protein" /db_xref="G1:13488605" /db_xref="G1:13488605" /translation="MSYVEDEDSHAELGEGPHWDVATONLYYDDINAGKLLRYNYN ENKYYKAKIEGEDLAGFAVFVEGTDGFAVGSGRRYVIVQWGGVSETAKVKTLFEVO TGDEBFTGARRENGENEVAFGAGTARYVEDGEGPEVTKSDVG ISNGLAWNBETTAKFYYDTOPYEVEYOFDEFAFGAGTARYFENGGEPTKSBOWG ISNGLAWNBETTKKFYYTGLGAKGYPMTKIQL" SRFGBPHPAGTTYKYTGLGAKGYPMTKIQL" SRFGBPHPAGTTYKYTGLGAKGYPMTKIQL"  Query Match  Query

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                                                                                                                                                                                                                                                                AF326959 992 bp mRNA linear INV 08-MAY-2001
Calliphora vicina anterior fat body protein (AFP) mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 992)
Hansen, I.A., Meyer, S.R., Berlinger, M.J. and Scheller, K.
Dlowfly Calliphora vicina
Unpublished
                                                                  156 TAAAGTAGATAAACTGGTTTCTTTCATTATTCCCCTTGCTGGATCCCCTGGCCGTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TGAAGGIGAGGATTTAGCTGGTTTTGCTGTGCCCGTCGAAGGTACAACCGATCAATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AGTCAGTTTGGAACGTGAAATAGCCATTCTTACATGGGATGGCGTTAGTGCTGCACCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 AAGCATAGAAGCTATTGTTAATGTCGAACCACATTAAAAAAT-----AACAGACT
TTATTAAAATCAGTACCCAACAACGGAAGTGTTACTGGATACCGTAAAAATACCAGATC
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Wuerzburg,
Germany
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Submitted (07-DEC-2000) Zoologie 1, University of Wuerzbur Submitted (07-DEC-2000) Zoologie 1, University of Wuerzbur Biocenter Hubland, Wuerzburg 97074, Germany

Location/Qualifiers

1. 992
//db_xref="taxon:7373"
//db_xref="taxon:7373"
//dev_stage="fat_body"
//dev_stage="larvae"

1. 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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Pred. No. 4.2e-12;
0; Mismatches 310; Indels
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onkvykakiegelfasfilpyenkpgefavcgclrpylvymgvsavakytfilebyd
pdlkbrrlinbktdpwrfycgrmadsgolfydwycellyswqsgcpnairskvgisn
glamyyrakkfrfyfonnhgylaydyngstgavsnpkvifdlkripeggplepdgmy
DDGNIYVAFPNGGTVPKVNPSTGKILLEIKIPTTQITSVAFGGPNLDILYVTANKF
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     Submitted (01-JUL-1999) Shin G Goto, Ohio State University, Department of Entomology; 1735 Neil Avenue, Columbus, OH 43210, USA (E-mail:shingoto@sci.osaka-cu.ac.jp, Tel:+1-614-292-4477, Fax:+1-614-292-2180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 TIGGAGAAGGICCICACIGGGAICAIGAAACICAGACCITAIAITICGICGACACCGIAG 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                        /product="senescence marker protein-30 (SMP-30)"
/protein_id="BAA92938.1"
/db_xreff="G1:7339662"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                   /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93.8; DB 3;
Pred. No. 8.3e-13;
0; Mismatches 382;
                                                                                                                                /strain="Canton S"
/db_xref="taxon:7227"
/tissue_type="whole body"
/dev_stage="7 day adult stage"
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llarity 48.8%;
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AB036903 1155 bp mRNA linear INV 12-JUL-2000 Sarcophaga peregrina AFP mRNA for anterior fat body protein, complete cds.
AB036903 1 G1:8980620
AB036903.1 G1:8980620
AFP; anterior fat body protein.
Sarcophaga peregrina larva fat body cDNA to mRNA.
Sarcophaga peregrina larva fat body cBNA to mRNA.
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
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Nakajima,Y and Natori,S.
Identification and characterization of an anterior fat body protein
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                                                                                          Gaps
                                                                                          12;
                                                               Length 1216;
                                                                                          Indels
                                                                                          292;
                                                                Score 90.4; DB 6;
Pred. No. 5.8e-12;
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                                                                                        0; Mismatches
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J. Biochem. 127 (5), 901-908 (2000)
20250851
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 /organism="Rattus sp."
/db_xref="taxon:10118"
. 231 c 309 g
                                                                9.8%;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                           CAATGATGGCAAGTGTGATCCTCGTGGTCGTTGTTTGCCGGTACCATGCGTTATGTCGG
                                                                                                                                                      339 TGAGGTAATCAAATCGGATGTGGGTATTTCCAATGGTTTGGCTTGGAATGAAGACAAAA
                                                                                                                                                                                                         - CAATGGCCATTCCATCTACAAATTAATCCCACCACGGCCAAGTTTTGTTGGAAATC--
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                                                                                                                                                                                          GAAAATGTATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTC
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                                      CAATGATGGCAAAAGCAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGC
                                                                                      387 TGGTCTCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGT
                                                                                                                                                                                                                                                                                               GCCTGGATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTT
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Yamaquchi, M.
Yamaquchi, M.
Patent: JP 1995123985-A 1 16-MAY-1995;
YAMAQUCHI MASAYOSHI, DAI ICHI PURE CHEM CO LTD
OR Rattus sp. (Rat)
PN JP 1995123985-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Rattus sp.'
80. 979
Tocation/Qualifiers
1. 1216
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C12N15/09,C12N1/21,(C12N1/21,C12R1:19);
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1993 JP 1993279349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
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E09237.1 GI:22025863
JP 1995123985-A/1.
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E09237
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/translation="MSSIKIECVLRENYRCGESPVWEEASKCLLFVDIPSKTVCRWDS
ISNRVQRVGVDAPVSSVALRQSGGVATIGTKFCALNWEDGSVFILAMVDEDKKNNRF
NDGKVDDAGRYFAGTMARETARAVLERHQGSLYSLFPDHSVKKYFNQVDISNGLDMSL
DHK IFYY IDSLSYTWDAFDYDLPTGQISNRRTVYKMENEGTPDGMCIDVEGKLWVAG
NGGRVIRLDPETGKRLQTVKLPVDKTTSCCFGGKDYSEMYVTCARDGMSAEGLLRQP
                                                                                                                                                                                                                                                                                                                             08-FEB-1999
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                                                                                                                                          TACCAGATCCTCAGGTCACCTCTGTAGCATTTGGCGGTCCGAATTTGGATGAACTGCATG 805
        685
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
     GATATCCAGATGGTCAAACAATTGATGAGGAGGGTAATTTATGGGTTGCCGTTTTCCAAG
                                                                                                                                                                 Gaps
                                                                          GACAGCGAATTATTAAAATCAGTACCCAACAACCGGAAGTGTTACTGGATACCGTAAAAA
                                                                                                          GTTATACCATCTACAAAGTTAATCCCACTACCGGTAAAGTTTTGTTGGAAA---TTTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Dec 8, 1994 this sequence version replaced gi:391851.
D16386:Submitted(07-Jun-1993)to DDBJ by: Masayoshi Yamaguchi.
Masayoshi Yamaguchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                calcium-binding protein; regucalcin.
Rattus norvegicus (strain:Wistar) liver cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (sites)
Shimokawa, N. and Yamaguchi, M.
Shimokawa, N. and Yamaguchi, M.
Molecular cloning and sequencing of the cDNA coding
calcium-binding protein regucalcin from rat liver
FEBS Lett. 327 (3), 251-255 (1993)
                                                                                                                                                                                                                                                                                                               Rat mRNA for calcium-binding protein, complete cds. D38467 D14327 D16386 D38467.1 GI:600378
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50.1%; Pred. No. 1.4e-11;
ive 0; Mismatches 293;
                                                                                                                                                                                                             806 TAACATCTGCTGGTCTTCAGCTTGACGACAGTTCT 840
                                                                                                                                                                                                                                 TCACAACATCTTCCCGTTTTGGTGAACCCGATCCT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graduate School of Nutritional Sciences University of Shizuoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="regucalcin"
/protein_id="BAA07490.1"
/db_xref="G1:408807"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAGNIFKITGLGVKGIAPYSYAG'
1154. .1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1594)
Shimokawa, N. and Yamaguchi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="liver
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/codon_start=1
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BASE COUNT 4:
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Best Local S
Matches 306
                                              726
                                                                               989
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              626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 GCAAGGCTACAAATCCCAAGGTTGTTTTCAATCTACGCAAAAATAGTCCCAAGGATCATC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 TATCCATCAGCAATCAACGGCCATTATTTACTTTTGAAAAGCAT-----GAAGTGCCTG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AGAAAACTTTTCATAAATATGTACCTTCTCAGAAA----AATACACGTTTTGTAAAG 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 ATGGCAAAGCAGATCCCCTTGGCAATCTATGGACAGGTACAATGGCTATTGACGCTGGTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 TCCCCGTAGGACCGGTCACTGGCAGTTTATATCATTTAGGGGCTGATAAAAAGGTAAAAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAATTCGAACATCGTTATGGTGAATTGTACAAATACGAAAAAGGTGGCAAAATTGAGG 545
                                                   Lab.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 TGTATTATATTGATTCGGGGAAAAGAAGAGTAGACGAGTACGATTATGATGCTTCTACAT
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                                                 Riken, Natori Special
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                               Submitted (06-JAN-2000) Yuki Nakajima, Riken, Natori Spe
Hirosawa2-1, Wako, Saltama 351-0198, Japan
(E-mail:nyuki@postman.riken.go.jp, Tel:+81-048-467-9439,
Fax:+81-048-462-4693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89.8; DB 3;
Pred. No. 8.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 382;
                                                                                                                                                 /organism="Sarcophaga peregrina"
/db_xref="taxon:7386"
/tissue_type="fat body"
/dev_stage="larva"
                                                                                                                   Location/Qualifiers
2 (bases 1 to 1155)
Nakajima,Y. and Natori,S.
Direct Submission
Submitted (06-JAN-2000) Y
                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.78;
                                                                                                                                                                                                                                      /gene="AFP"
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/traislation="MSSIKIECVLRENYRCGESPVWEEASKCLLEVDIPSKTVCRWDS
ISNRVQRVGVDAPVSSVALRQSGGYVATIGTKFCALNWEDQSVFILAMVDEDKKNNRR
NDGKVDPARYRGTRARETARAVLEHQGSLYSLFPDHSVKKYFDOVDISNGLDWSL
NDGKYDPARYRGTRAFDYDLPTGOISNRFVYKMEKDEOIPDGMCIDVEGKLWVAC
YNGGRYIRLDPETGRELQTVKLPVDKTTSCCFGGKDYSEMYVTCARDGMSAEGLLRQP
DAGNIFKITGLGVKGIAPYSYAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 AGAAGAGTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           778 ACAGGGAAA---AGACTGCAAACTGTGAAGTTGCCTGTTGATAAAACAACTTCATGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        775 TTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        835 AGTTCTTTNGACAAAAGTTTAGTTAATGGGCACGTCTACAGAGTAACAGGTTTAGGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1594;
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                                                                                                            protein-30"
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85.6; DB 10;
Pred. No. 9e-11;
0; Mismatches 295;
                                                                                                            /product="senescence marker
                                                                                                                         /protein_id="CAA48786.1"
/db_xref="G1:57255"
/db_xref="SWISS-PROT:Q03336"
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    /db_xref="taxon:10116"
                   /dev_stage="6 months'
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1588
                                              /gene="SMP30"
88. .987
                                                                              /gene="SMP30"
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al Similarity 49.8%;
304; Conservative
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Sakaecho, Itabashi-ku,
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                                               CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGGTA---GGACCGGTCACTGGC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Fujita,T., Shirasawa,T., Uchida,K. and Maruyama,N.
Isolation of CDNA clone encoding rat senescence marker (SMP30) and its tissue distribution
Biochim. Biophys. Acta 1132 (3), 297-305 (1992)
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35-2,
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/strain="Wistar/Sic"
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Direct Submission
Submitted (08-DEC-1992) T. Fujita,
.'':t-n Inst. of Gerontology,
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Tokyo 173, JAPAN
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/translation="MSSIKVBCULRENYRCGESPVWBEASOSLLFVDIPSKIICRWDT
VSNOVQRVAVDAPVSSVALRQLGGYVATIGTRFCALNWENOSSFVLAMVDEDKKNNRF
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YNGGRVIRLDPETGKRLQTYKLPYDKTTSCCFGGKDYSEMYVTCARDGLNAEGLLRQP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.mus
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Submitted (24-JUN-1996) Masayoshi Yamaguchi, University of
Submitted (24-JUN-1996) Masayoshi Yamaguchi, University of
Shizuoka, Laboratory of Endocrinology and Molecular Metabolism,
Graduate School of Nurtritional Sciences; 52-1 Yada, Shizuoka,
Shizuoka 422, Japan (Tel.104-264-5580, Fax:054-264-5580)
Sequence updated (15-Jul-1996) by: Masayoshi Yamaguchi.
Location/Qualifiers
                    715 CAACCGGAAGIGITACIGGAIACCGIAAAAAIACCAGAICCICAGGICACCICIGIAGCA
                                                                                                                                                  775 TTTGGCGGTCCGAATTTGGATGAACTGCATGTAACATCTGCTGGTCTTCAGCTTGACGAC
GAGGGTAATTTATGGGTTGCCGTTTTCCAAGGACAGCGAATTATTAAAATCAGTACCCAA
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Murata,T. and Yamaguchi,M.
Molecular cloning of the cDNA coding for regucalcin and
expression in mouse liver: the expression is stimulated
administration
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Mus musculus liver CDNA to mRNA.
Mus musculus
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/db_xref="taxon:10090"
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/protein_id="BAA13046.1"
/db_xref="GI:1483152"
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207 c 282 g 31
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ISNRVQRVGVDAPVSSVALRGSGGYVATIGTKFCALNWEDGSVFILAMVDEDKKNNRF
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DHKIFYYIEDSLSYTVDAFDYDLPTGOISNRRTVYKMEKDEGIPDGMOIDVEGKLWVAC
YNGGRYTRLDPETGERLAGTVKLPVDKTTSCCFGGKDYSEMYYTCARDGMSAEGLLRQP
DAGNIFKITGLGVKGIAPYSXAG"
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                      Misawa, H. and Yamaguchi, M. The gene family encoding the calcium-binding protein regucalcin Unpublished
                                                                                                                                                                                                                                                                                                                                                                                              of
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Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School
Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School
Nutritional Sciences, University of Shizuoka, Laboratory of
Endocrinology and Molecular Metabolism; 52-1 Yada, Shizuoka
422-8526, Japan (E-mail:yamaguchéfnsl.u-shizuoka-ken.ac.jp,
Tel:+81-54-264-5580, Fax:+81-54-264-5580)
Location/Qualifiers
                                                                                                                                                    Rattus norvegicus hepatoma cell_line:H4-II-E cDNA to mRNA.
Rattus norvegicus
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Pred. No. 9e-11;
0; Mismatches 295;
                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="H4-II-E"
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/protein_id="BAA90692.1"
/db_xref="G1:6970313"
                                                                 1605 bp
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99. .998
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Yamaguchi,M. and Misawa,H.
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                                                                                     norvegicus mRNA
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al Similarity 49.8%;
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JOURNAL
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VSNQVQRVAVDAPVSSVALRQLGGYVATIGTRFCALNWENQSVFVLAMVDEDKKNNRF
NDGRVDPAGRYFAGTMAEETAPAVLERHQGSLYSLFPDHSVKKYFDQVDISNGLDWSL
DHKIFYYIDSLSYTVDAFDYDLQTGOISNRRIYYKMEKDEQIPDGMCIDAEGKLWVAC
YNGGRVIRLDPETGKRLQTVKLPVDKTTSCCFGGKDYSEMYVTCARDGLNAEGLLRQP
DAGNIFKITGLGVKGIAPYSYAG"
1132. .1137
                                                                                                                                                          /translation="MSSIKVECVLRENYRCGESPVWEEASQSLLFVDIPSKIICRWDT
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                                                                                                            protein-30"
                                                                                                                                                                                                                                                                                                                                                     Score 80.8; DB 10;
Pred. No. 1.4e-09;
0; Mismatches 298;
                                                                                                           /product="senescence marker
                                                                                                                         /protein_id="AAC52721.1"
/db_xref="GI:1144000"
    /tissue_type="liver"
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                    /dev_stage="adult"
1. .1573
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/gene="SMP30"
1551. .1556
                                            /gene="SMP30"
73 972
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/gene="SMP30"
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Fujita,T., Shirasawa,T. and Maruyama,N.
Fujita,T., Shirasawa,T. and Maruyama,N.
Fisolation and characterization of genomic and cDNA clones encoding mouse senescence marker protein 30 (SMP30)
Blochim. Biophys. Acta 1308 (1), '49-57 (1996)
                                                                                                                                                                                                                                                                                                   GTTTACAAGATGGAAAAAGATGAA-----CAAATCCCAGATGGAATGTGCATTGATGCT
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                               CTATGGACAGGTACAATGGCTATTGACGCTGGTCTCCCCGTA---GGACCGGTCACTGGC
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Submitted (10-JUN-1995) Takuji Shirasawa, Molecular Pathology,
Tokyo Metropolitan Institute of Gerontology, 35-2, Sakaecho,
Itabashi-ku, Tokyo 173, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57Black/6"
/db_xref="taxon:10090"
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Shirasawa, T.
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                                                                                                                                                                                                                                                                                                                                                                715 CAACCGGAAGTGTTACTGGATACCGTAAAATACCAGATCCTCAGGTCACCTCTGTAGCA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           775 IIIGGCGGICCGAAIIIGGAIGAACIGCAIGTAACAICIGCIGGICIICAGCIIGACGAC 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 TCCTTGTACTCCCTCTTTCCTGATCACAGTGTGAAAAATACTTTGACCAAGTGGATATC 541
                                                                                                                                                                                                                                                                                   662 GTTTACAAGATGGAAAAAGATGAA-----CAAATCCCAGATGGAATGTGCATTGATGCT
                                                                                                                                                                                     602 TACACTGTGGGATGCCTTTGACTATGACCTACAAACAGGACAGATTTCCAACGCAGAATT
                                                                                                                                                                                                                                       595 TTATTTACTTTTGAAAAGCATGAAGTGCCTGGATATCCAGATGGTCAAACAATTGATGAG
                                                                                              542 TCCAATGGTTTGGATTGGTCCCTGGACCATAAAATCTTCTACTACATTGACAGCCTGTCC
                                                                                                                                             535 AGAAGACTAGACGAGTACGATTATGATGCTTCTACATTATCCATCAGCAATCAACGGCCA
                                                 475 GCAAATGGGCTCGCGTGGAGTAATGATTTGAAGAAAATGTATTATATTGATTCGGGGAAA
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DHKIFYYIDSLSYTVDAFDYDLGAGISNRRIVYKMEKDEQIPDGMCIDAEGKLDNSC
DHKIFYYIDSLSYTVDAFDYDLGAGISNRRIVYKMEKDEQIPDGMCIDAEGKLWAC
PROGRYIRLDPETGRRLQTYKLPVDKTTSCCFGGKDYSEMYYTCARDGLNAEGLLRQP
DAGNFKITGLGVKGIAPYSVG"
1 293 c 370 g 469 t
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VSNQVQRVAVDAPVSSVALRQLGGYVATIGTKFCALNWENQSVFVLAMVDEDKKNNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found
                                BC012710 . 1598 bp mRNA linear ROD 07-AUG-2002
Mus musculus, Similar to regucalcin, clone MGC:14006 IMAGE:4210374,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 GTGGATGAAGATAAGAAAATAATCGATTCAATGATGGGAAGGTGGATCCTGCTGGGAGA 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: n Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677738. Location/Qualifiers
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1598)
                                                                                                                                                                                                                                                                                                                                               Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.systemsbiology.org
context: amadanfsystemsbiology.org
Anup Madan, Jossica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Liver, normal. 5 month old male mouse. /clone_lib="NOI_CGAP_Li9" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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Pred. No. 1.4e-09;
0; Mismatches 298; Indels 12;
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/protein_id="AAH12710.1"
/db_xref="GI:15215231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="MGC:14006 IMAGE:4210374"
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86, .985
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//organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
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Best Local Similarity 49.33
Matches 301; Conservative
                                                                                         mRNA, complete cds
BC012710
                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                       Strausberg, R.
                                                                                                                                                                                                              Mus musculus
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ORIGIN
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AUTHORS
TITLE
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                                                                                                               ACCESSION
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KEYWORDS
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